

Query Match 11.7%; Score 83; DB 7; Length 192;
Best Local Similarity 28.8%; Pred. No. 0.89;
Matches 30; Conservative 11; Mismatches 31; Indels 32; Gaps 5;
QY 22 EDVMEALLRVKSSERLAMLRLAG-----MCHRVLPDGTGASAIATVTPKQASM 72
DB 112 FDCFSDSAIR-----KALLGHIIVSPCEYQAGHNKVSQYLALALITPK----- 157
QY 73 KLPKPPPOSTKSPLELSRKIRENMNKTISOESARVNHRLPEGH 116
DB 158 KIKPLPSPVTKLTEDR-----WNKPKTKGHRGSHRI-NGH 192

RESULT 4
AAU03538
ID AAU03538 standard; Protein; 945 AA.
XX
AC AAU03538;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human protein kinase #39.
XX
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder.

XX Homo sapiens.
XX WO200138503-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US32085.
XX
XX 24-NOV-1999; 99US-0167482.
XX
XX (SUGEN-) SUGEN INC.
XX
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX Flanagan P, Clary D;
XX
XX WPI; 2001-343950/36.
XX
XX N-PSDB; AAS06738.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
XX diagnosing and/or treating e.g. cancer, immune, cardiovascular and
XX neuronal-associated diseases, and microbial infections -
XX
XX Claim 7; Figure 2; 433pp; English.

XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The
XX novel protein kinases have been identified as members of the tyrosine
XX or serine/threonine kinase (PTK and STK) families. The polynucleotides
XX encoding protein kinases and the polypeptides may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate kinase expression. For example, they may be used to treat
XX cancers (especially cancers of haematopoietic origin), cardiovascular
XX disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
XX immune related diseases (e.g. rheumatoid arthritis), neurological
XX disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
XX Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
XX disease (e.g. HIV) and reproductive disorders (e.g. infertility).
XX Additionally, polynucleotides encoding protein kinases may be
XX used for gene therapy and as DNA probes in diagnostic assays.
XX The protein kinase polypeptides may be used as antigens in the production
XX of antibodies against the protein kinases and in assays to identify
XX modulators of protein kinase expression and activity.

XX Sequence 945 AA;

Query Match 11.5%; Score 81.5; DB 22; Length 945;
Best Local Similarity 28.3%; Pred. No. 10;
Matches 30; Conservative 14; Mismatches 37; Indels 25; Gaps 5;
QY 43 ALAGMC-----GHRVLPOTGASA-----IAATVTPKGA-----SMKLKPPRP 79
DB 226 AYPGLCPPLPESGHRSLPPSPQRHVAVRTPPTPNIVTTVTPGTPPMKKNKLKPPGT 285
QY 80 QSTKSPLELSRKIRENMNKTISOESARVNHRLPEGH-PLEKRAE 124
DB 286 PPSRSRKLHLIFGFTALHRSKSHF-FQGHRYVDEAHTPKAKKSK 330

RESULT 5
AAE19157
ID AAE19157 standard; Protein; 945 AA.
XX
AC AAE19157;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human kinase polypeptide (PKIN-15).
XX
KW Human; kinase polypeptide; PKIN-15; gene therapy; Addison's disease;
KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
KW cholestasis; cardiast; cardiovascular disorder; Niemann-Pick's disease;
KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
KW hypotensive; anti-HIV; enzyme.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 661..920
XX FT /note= "Eukaryotic protein kinase domain"
XX
XX WO200208399-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US23092.
XX
XX 21-JUL-2000; 2000US-220038P.
XX 28-JUL-2000; 2000US-222112P.
XX 04-AUG-2000; 2000US-222831P.
XX 11-AUG-2000; 2000US-224729P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX (THOR/) THORNTON M.
XX
XX Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK;
XX Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
XX Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P;
XX Ding L, Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM;
XX Greenwald SR, Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J;
XX Hillman JL;
XX WPI; 2002-206083/26.
XX N-PSDB; AAD30562.
XX
XX New human kinase polypeptide, useful in diagnosis, prevention and
XX treatment of cancer, immune disorder, growth and developmental
XX disorder, cardiovascular disorder and lipid disorder -
XX
XX Claim 1; Page 155-157; 196pp; English.

XX The present invention relates to an isolated human kinase polypeptide
XX (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
XX useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
XX lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency

CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
CC buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
CC drug screening techniques and to analyse the proteome of a tissue or cell
CC type. PKIN is useful for creating knockin humanised animals or transgenic
CC animals to model human diseases, in somatic or germline gene therapy, to
CC generate a transcript image of a tissue or cell type, for detecting
CC differences in the chromosomal location due to translocation, inversion,
CC etc., among normal, carrier or affected individuals, and as hybridisation
CC probes for mapping naturally occurring genomic sequences. PKIN is useful
CC in southern or northern analysis, dot blot or other membrane-based
CC technologies, in PCR technologies, in dipstick, pit, multifomat enzyme
CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
CC fluids or tissues from patients to detect altered PKIN expression. The
CC present sequence is human PKIN-15.
XX
XX Sequence 945 AA;
SQ
Query Match 11.5%; Score 81.5; DB 23; Length 945;
Best Local Similarity 28.3%; Pred. No. 10;
Matches 30; Conservative 14; Mismatches 37; Indels 25; Gaps 5;
QY 43 ALAGMC-----GHRVLPCTGASA-----IAATVTPKGA-----SMKLPKPRP 79
Db 226 AYPGLCPPLPPLSGHSLPSRQRAVHTPPTPNVITVTPTTPPMRKNKLPKPT 285
QY 80 QSTKSPRLRLSRKREMNKTIQSARVNHRLPUGH-PLLEKRAE 124
Db 286 PPPSSRKLIHLIPGFTALHRSKHE-FQGHVRVDEAHTPKAKKSK 330
RESULT 6
ABG61917
ID ABG61917 standard; Protein; 1259 AA.
XX AC ABG61917;
XX
XX 15-AUG-2002 (first entry)
XX
XX Prostate cancer-associated protein #118.
XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX Mammalia.
XX WO200230268-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US32045.
XX
XX 13-OCT-2000; 2000US-0687576.
XX 08-DEC-2000; 2000US-0733288.
XX 08-DEC-2000; 2000US-0733742.
XX 24-JAN-2001; 2001US-263957P.
XX 16-MAR-2001; 2001US-276791P.
XX 16-MAR-2001; 2001US-276888P.
XX 06-APR-2001; 2001US-281922P.
XX 24-APR-2001; 2001US-286214P.
XX 30-APR-2001; 2001US-0847046.
XX 04-MAY-2001; 2001US-288589P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI; 2002-471335/50.
XX N-PSDB; ABK92234.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a

PT patient, useful for diagnosing prostate cancer (PC) or screening
PT modulators of PC, by determining if prostate cancer-associated genes
PT are expressed in a prostate tissue
XX
XX Claim 27; Page 401; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABG61800-ABG61944 represent prostate cancer-associated proteins.
XX
XX Sequence 1259 AA;
SQ
Query Match 11.5%; Score 81.5; DB 23; Length 1259;
Best Local Similarity 26.8%; Pred. No. 14;
Matches 37; Conservative 17; Mismatches 43; Indels 41; Gaps 6;
QY 20 ETFDVMEALLRVKSSRLAMLR-----LAGMCHRVLPCTG-----ASAIA 62
Db 655 EQLDAINKEIRLIQEEKESTELRAEINERVASVLEGLNARVHPTCSITASVTASSLA 714
QY 63 ATVTPKGASM-KLKPRPQ-----STKSPRLRLSRKI-----RMNKTISOESA 106
Db 715 SSSPPSGHSTPKLTPSPAREMDRMGMVTLPDLRKHRRXIIVVEEDGREDKATIKETS 774
QY 107 -----RVNHLPEGH 116
Db 775 PPPTPRALRMTHTLPSSY 792
RESULT 7
ABG63351
ID ABG63351 standard; Protein; 1157 AA.
XX AC ABG63351;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 16845.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL07454.
XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX Disclosure; SEQ ID NO 16845; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU16051), expressed DNA
CC sequences (ABU1640-ABU16175) and the encoded proteins
CC (ABU57737-ABU72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 1157 AA;
SQ
Query Match 11.4%; Score 80.5; DB 22; Length 1157;
Best Local Similarity 28.4%; Pred. No. 17;
Matches 25; Conservative 13; Mismatches 37; Indels 13; Gaps 3;
QY 55 GTGAGATATVTPKGAS--MKLKPRP-----QSTKSPPELRLSR--KIREMNKTI 101
Db ||| : : : : : ||| : : : : : ||| : : : : :
462 GTGTGDRYSRPTSTSRVMSSESPSPVSGSGHHYHRRSPRMRQTRGDSRRSPSSA 521
QY 102 SOESARVNHRLPECHPLLEKRAEYFHL 129
Db ||| : : : : : ||| : : : : : ||| : : : : :
522 SSESASRSRSPTRDLKHKREYIKKI 549
RESULT 8
AY01973
ID AAY01973 standard; Protein; 192 AA.
XX AC AAY01973;
XX DT 02-JUL-1999 (first entry)
XX DE HIV-1 viral infectivity factor protein N23.
XX KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
XX viral infectivity factor; HIV-1; vaccine.
XX OS Human immunodeficiency virus type 1.
XX PN WO9913896-A1.
XX PD 25-MAR-1999.
XX PF 18-SEP-1998; 98WO-US19478.
XX PR 26-SEP-1997; 97US-0060172.
XX PR 18-SEP-1997; 97US-0059283.
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX PI Ayyavoo V, Nagashunmugam T, Weiner DB;
XX WPI; 1999-263380/22.
XX DR N-PSDB; AAX35221.
XX CC New attenuated vif (viral infectivity factor) genes, used in genetic
XX vaccines against HIV-1
XX Claim 2; Page 63; 92pp; English.
XX The specification describes novel vif proteins (AAY01969-88) and
XX the genes encoding them (AAX35217-36). The vif gene is an accessory gene
XX for HIV-1 that has low functional mutagenicity and is conserved. In
XX addition, attenuated, non functional vif clones are able to induce

CC immune responses capable of destroying native pathogen. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include
CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.
XX Sequence 192 AA;
SQ
Query Match 11.2%; Score 79; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 2.4;
Matches 32; Conservative 9; Mismatches 28; Indels 38; Gaps 6;
QY 22 FVMEALLRVKSSERLAWLRALAGMCHRVLP---GTGAS-----AIAATVTPKG 69
Db ||| : : : : : ||| : : : : : ||| : : : : :
112 FDLSESAR-----KAILGHRVSPCEYRAGSKVGSLOYLAIALIITPK- 157
QY 70 ASMKLKPPRPOSTKSPPELRLSRKIREMNKTIISOESARVNHRLPEGH 116
Db ||| : : : : : ||| : : : : : ||| : : : : :
158 ---KIKPLPSVRKLTEDR-----WNKPKTKGHRGSHTM-NGH 192
RESULT 9
ABU53201
ID ABU53201 standard; Protein; 1780 AA.
XX AC ABU53201;
XX DT 14-APR-2003 (first entry)
XX DE Human cell cycle-associated protein from DKFZphtes3_35b4.
XX KW Human; gene therapy; vaccine; disease treatment; detection.
XX OS Homo sapiens.
XX PN WO200112659-A2.
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000WO-IE01496.
XX PR 18-AUG-1999; 99US-0149499.
XX PR 28-SEP-1999; 99US-0156503.
XX PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX PI Wiemann S;
XX WPI; 2001-327840/34.
XX DR N-PSDB; ABX71393.
XX CC Nucleic acids having the sequences of clones isolated from libraries of
XX different human tissues, useful in recombinant DNA methodologies -
XX Claim 21; Page 821; 1095pp; English.
XX This invention describes novel polynucleotides and polypeptides isolated
XX from human cDNA libraries which can be used for gene therapy or in
XX vaccines. The polynucleotides of the invention and antibodies encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate polypeptide expression. The products of the
XX invention may also be used to identify modulators of expression and
XX activity and to down regulate expression and activity. The antibodies of
XX the invention may also be used as diagnostic agents for detecting the
XX presence of polypeptides in samples. This sequence represents a
XX polypeptide described in the disclosure of the invention.
XX Sequence 1780 AA;
SQ
Query Match 11.2%; Score 79; DB 22; Length 1780;
XX

Best Local Similarity 21.3%; Pred. No. 42; Mismatches 27; Indels 14; Gaps 2; Matches 32; Conservative 77; Indels 14; Gaps 2;

QY 2 ESTSTTTNFAENRPTFGTDFVMDREALLRVKSSERLAMLRLALAGMCHRVLPOTGASAI 61
Db 604 EVTQFTQYWAQREADFKETLLQERE-ILEENAERRLAIFKDLVGVKCDTREAAKDICAT 662
QY 62 AATVTPKGASMKLPKPPRPOSTKSPELRELSRKIREMNKTSIQESARV----- 108
Db 663 KVETEATACLKFNQIKAEALAKTKGELIKTKRENESSDLSIQELETNSKKIITQ 722
QY 109 NHRLPFGHPLLEKRAEYFRHLRLSKSQGVN 138
Db 723 NQRIKELINIIDQKEDTINEFQNLKSHMEN 752

RESULT 10
AAM38681
ID AAM38681 standard; Protein; 1780 AA.
XX
AC AAM38681;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 1826.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI57837.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 3; SEQ ID NO 1826; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 1780 AA;
Query Match 11.2%; Score 79; DB 22; Length 1780;
Best Local Similarity 21.3%; Pred. No. 42;
Matches 32; Conservative 77; Mismatches 77; Indels 14; Gaps 2;

QY 2 ESTSTTTNFAENRPTFGTDFVMDREALLRVKSSERLAMLRLALAGMCHRVLPOTGASAI 61
Db 604 EVTQFTQYWAQREADFKETLLQERE-ILEENAERRLAIFKDLVGVKCDTREAAKDICAT 662
QY 62 AATVTPKGASMKLPKPPRPOSTKSPELRELSRKIREMNKTSIQESARV----- 108
Db 663 KVETEATACLKFNQIKAEALAKTKGELIKTKRENESSDLSIQELETNSKKIITQ 722
QY 109 NHRLPFGHPLLEKRAEYFRHLRLSKSQGVN 138
Db 723 NQRIKELINIIDQKEDTINEFQNLKSHMEN 752

RESULT 11
AAM40467
ID AAM40467 standard; Protein; 1788 AA.
XX
AC AAM40467;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5398.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59623.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX

PT responsible for genetic disorders or other traits and to assess
 XX biodiversity -
 PS Claim 20; SEQ ID No 59462; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 828 AA;

Query Match 11.1%; Score 78.5; DB 22; Length 828;
 Best Local Similarity 24.0%; Pred. No. 18;
 Matches 24; Conservative 16; Mismatches 41; Indels 19; Gaps 2;
 QY 4 TTTTNFVAENRPTGTTFDVNRALLRVKSSERLAMLALAGMCGHRVLPOTGASAIYAA 63
 DB 228 TDTTTLRVIRLGAVGSDLEKVRKVLKAAATGHRVPM-----HSPMPEVFTAFGA 278
 QY 64 TVTPKGASKMLKPPRQSTKSPELRELSRKIREMKNKTISQ 103
 DB 279 STLDHRLYVR-----ELDRSRSTVDLNRITDQ 308

RESULT 14
 AAP60348
 ID AAP60348 standard; protein; 203 AA.
 XX
 AC AAP60348;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-JAN-1980 (first entry)
 XX
 DE HTLV-III virus (HIV virus) sor protein.
 XX
 KW HTLV-III; HIV virus; AIDS; active immunization; sor protein;
 KW passive immunization; vaccine; ss.
 XX
 OS HIV virus (HTLV-III).
 XX
 PN EP185444-A.
 XX
 PD 25-JUN-1986.
 XX
 PF 10-OCT-1985; 8SEP-0307260.
 XX
 PR 23-JAN-1985; 85US-0693866.
 PR 10-OCT-1984; 84US-0659339.
 XX
 PA (CENZ) CENTOCOR INC.
 PA (USSH) NAT INST OD HEALTH.
 XX
 PI Chang NT;
 XX
 DR WPI; 1986-163443/26.

DR N-PSDB; AAN60240.
 XX
 PT New immunoreactive HTLV-III polypeptide expressed by transformed
 PT cells - and derived antibodies, useful for diagnosis of AIDS and
 PT in active or passive immunisation
 XX
 PS Disclosure; Fig. 3; 60pp; English.
 XX
 CC HIV virus cDNA is cleaved with restriction endonucleases to produce
 CC the gag protein. The resulting protein and antibodies against it
 CC are useful for immunosay of HIV virus, e.g. by sandwich type RIA.
 CC The protein may also be used in vaccines for active immunization.
 CC See also AAP60346-7 and AAP60349.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 203 AA;

Query Match 11.0%; Score 78; DB 7; Length 203;
 Best Local Similarity 27.9%; Pred. No. 3.3;
 Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
 QY 22 FDMVREALLRVKSSERLAMLALAG-----MCGHRVLPOTGASAIYAAATVTPKGASM 72
 DB 123 FDFPSDAIR-----KALLGHIVSPRCYQAGHNKVGSLQYLALALITPK---- 168
 QY 73 KLKPPRQSTKSPELRELSRKIREMKNKTISQESARVNHRLPEGH 116
 DB 169 KIKPPLPSVTKLTEER-----MKNPKQTKGHRGSHTW-NGH 203

RESULT 15
 ABB68134
 ID ABB68134 standard; Protein; 409 AA.
 XX
 AC ABB68134;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 31194.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL12237.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 31194; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 10.9%; Score 77.5; DB 22; Length 409;
Best Local Similarity 33.3%; Pred. No. 9.3;
Matches 26; Conservative 13; Mismatches 28; Indels 11; Gaps 3;

QY 59 SAIAATVTPKASMKLKPDPQSTKSPELRSLRKIREMNTKISQESARVNHRLPEGH 118
DB 14 AAVLMTATROGHTIRGPP-----GVARSLEGRIREENVDPVVARINIGFPQ---L 63

QY 119 LEKR-AYEVRHLRLSKSQ 135
DB 64 KESRSQALKRLEHLKXQ 81

RESULT 15
ABB83793
ID ABB83793 standard; Protein; 451 AA.
XX AC ABB83793;
XX DT 29-AUG-2002 (first entry)
XX DE Fungal decaprenyl diphosphate synthase SEQ ID NO 4.
XX KW Fungi; Aspergillus; Leucosporidium; coenzyme Q10; enzyme;
XX KW decaprenyl diphosphate synthase; enzyme.
XX KS Aspergillus clavatus.
XX PN WO200252017-A1.
XX PD 04-JUL-2002.
XX PF 27-DEC-2001; 2001WO-JP11523.
XX PR 27-DEC-2000; 2000JP-0398658.
XX PA (KANF) KANEKA CORP.
XX PI Matsuda H, Kawamukai M, Yajima K, Ikenaka Y;
XX DR WPI; 2002-500767/53.
XX DR N-PSDB; AEN81605.
XX DT Microbial production of coenzyme Q10 by transformants transferred with fungal decaprenyl diphosphate synthase gene, on industrial scale for application in drugs -
XX KS Claim 4; Page 37-40; 52pp; Japanese.
XX CC The invention relates to a DNA sequence (I, AEN81604-ABN81605), containing a sequence based on that of (I) but with some bases deleted, added, inserted and/or substituted and encoding a protein (ABB83792-ABB83793) with decaprenyl diphosphate synthase activity or hybridisable with (I) under stringent conditions and encoding a protein with decaprenyl diphosphate synthase activity. The DNA is useful for the production of coenzyme Q10 for application in drugs. The coenzyme is simply produced on industrial scale, efficiently, with significantly productivity.

QY Sequence 451 AA;
Query Match 10.9%; Score 77.5; DB 23; Length 451;
Best Local Similarity 29.6%; Pred. No. 10;
Matches 24; Conservative 12; Mismatches 28; Indels 17; Gaps 3;

QY 57 GASAIATVTPKASMKLKPDPQSTKSPELRSLRKIREMNTKISQESARVNHRLPEGH 116
DB 56 GAASAAQTIFKGL-----PKAPPGISVDPLRVGKELKFLTKNIHQ-----LLGSGH 103

QY 117 PLEKRAEYF-----RHLRSL 132
DB 104 PTLQKVAKYTRSEGHWRPL 124

RESULT 17
AAW94135
ID AAW94135 standard; peptide; 96 AA.
XX AC AAW94135;
XX DT 13-APR-1999 (first entry)
XX DE VIF-derived HIV protease inhibitor C'vif (residues 97-192).
XX KW Protease inhibitor; lentiviral; retroviral; replication; Vif protein; simian immunodeficiency virus; feline immunodeficiency virus; HIV-1; bovine immunodeficiency virus; infection; HIV-2.
XX OS Synthetic.
XX OS Human immunodeficiency virus type 1.
XX PN WO9852970-A1.
XX PD 26-NOV-1998.
XX PF 20-MAY-1998; 98WO-US10307.
XX PR 20-MAY-1997; 97US-0047200.
XX PA (SLUK-) ST LUKE'S ROOSEVELT HOSPITAL.
XX PA (YISS) YISSUM RES & DEV CO.
XX PI Kotler M, Volsky DJ;
XX DR WPI; 1999-059738/05.
XX PT New protease inhibitors comprising a sequence of lentiviral vif - which inhibit lentiviral replication, used for treating or preventing infection, particularly by HIV
XX PS Example 1; Page 31; 108pp; English.
XX CC The invention provides protease inhibitors which inhibit lentiviral or retroviral replication where the inhibitor comprises an amino acid sequence which corresponds to an amino acid sequence in a lentiviral vif protein. The protease inhibitors can be used for the prevention or treatment of lentiviral or retroviral infection, e.g. those resulting from HIV-1, HIV-2, simian immunodeficiency virus, feline immunodeficiency virus, bovine immunodeficiency virus. DNA encoding the peptides can also be used in such methods. The present sequence represents an example of a peptide inhibitor of the invention derived from the HIV-1 Vif protein.

QY Sequence 96 AA;
Query Match 10.9%; Score 77; DB 20; Length 96;
Best Local Similarity 27.9%; Pred. No. 1.6;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMVEALLRVKSSERLAMLALAG-----MCGRVLPPTGASAIATVTPKASGM 72
DB 16 FDFCSDAIR-----KALLGHIVSPCEVOAGHNKVGSLQYLALALITPK---- 61

QY 73 KLKPPRQSTKSPELRSLRKIREMNTKISQESARVNHRLPEGH 116
DB 62 KIKPLPSVTKLTEDR-----WNKPQKTKGHRSHMT-NGH 96

RESULT 18

AAY01976
 ID AAY01976 standard; Protein; 192 AA.
 XX
 AC AAY01976;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE HIV-1 viral infectivity factor protein N27.
 XX
 KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
 KW viral infectivity factor; HIV-1; vaccine.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9913896-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 18-SEP-1998; 98WO-US19478.
 XX
 PR 26-SEP-1997; 97US-0060172.
 PR 18-SEP-1997; 97US-0059283.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Ayyavoo V, Nagashunmugam T, Weiner DB;
 XX
 DR WPI; 1999-263380/22.
 DR N-PSDB; AAX35224.
 XX
 PT New attenuated vif (viral infectivity factor) genes, used in genetic
 PT vaccines against HIV-1
 XX
 PS Claim 2; Fig 7B-C; 92pp; English.
 XX
 CC The specification describes novel vif proteins (AAY01969-88) and
 CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
 CC for HIV-1 that has low functional mutagenicity and is conserved. In
 CC addition, attenuated, non functional vif clones are able to induce
 CC immune responses capable of destroying native pathogen. Vif nucleic
 CC acids may be used to immunize mammals. The attenuated, non-functional
 CC vif genes may be used in concert with other HIV-1 genes to produce
 CC vaccine that has a broad immune response against all viral
 CC components, and which mimics many aspects of the immune responses
 CC induced by a live attenuated virus. Prophylactic vaccines which include
 CC vif could limit both viral escape and contribute to lowering the viral
 CC set point during early infection stages.
 XX
 SQ Sequence 192 AA;
 Query Match 10.9%; Score 77; DB 20; Length 192;
 Best Local Similarity 29.9%; Pred. No. 4;
 Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
 QY 22 FDMREALLRVKSSERLAMLRLAGMCHRVLP-----GTGAS-----AIAATVTPKG 69
 Db 112 FDCFSESAR-----KAILGHRVSPRCEYRAGHSKVGSLQYLAIALITPK- 157
 QY 70 ASMKLKPPRQSTKSPLELSRKIREMNTISQESARVNHRLPEGH 116
 Db 158 ---KIKPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192
 RESULT 19
 AAY01977
 ID AAY01977 standard; Protein; 192 AA.
 XX
 AC AAY01977;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE HIV-1 viral infectivity factor protein N29.
 XX
 KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
 KW viral infectivity factor; HIV-1; vaccine.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9913896-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 18-SEP-1998; 98WO-US19478.
 XX
 PR 26-SEP-1997; 97US-0060172.
 PR 18-SEP-1997; 97US-0059283.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Ayyavoo V, Nagashunmugam T, Weiner DB;
 XX
 DR WPI; 1999-263380/22.
 DR N-PSDB; AAX35224.
 XX
 PT New attenuated vif (viral infectivity factor) genes, used in genetic
 PT vaccines against HIV-1
 XX
 PS Claim 2; Fig 7B-C; 92pp; English.
 XX
 CC The specification describes novel vif proteins (AAY01969-88) and
 CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
 CC for HIV-1 that has low functional mutagenicity and is conserved. In
 CC addition, attenuated, non functional vif clones are able to induce
 CC immune responses capable of destroying native pathogen. Vif nucleic
 CC acids may be used to immunize mammals. The attenuated, non-functional
 CC vif genes may be used in concert with other HIV-1 genes to produce
 CC vaccine that has a broad immune response against all viral
 CC components, and which mimics many aspects of the immune responses
 CC induced by a live attenuated virus. Prophylactic vaccines which include
 CC vif could limit both viral escape and contribute to lowering the viral
 CC set point during early infection stages.
 XX
 SQ Sequence 192 AA;
 Query Match 10.9%; Score 77; DB 20; Length 192;
 Best Local Similarity 29.9%; Pred. No. 4;
 Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
 QY 22 FDMREALLRVKSSERLAMLRLAGMCHRVLP-----GTGAS-----AIAATVTPKG 69
 Db 112 FDCFSESAR-----KAILGHRVSPRCEYRAGHSKVGSLQYLAIALITPK- 157
 QY 70 ASMKLKPPRQSTKSPLELSRKIREMNTISQESARVNHRLPEGH 116
 Db 158 ---KIKPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

XX
 KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
 KW viral infectivity factor; HIV-1; vaccine.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9913896-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 18-SEP-1998; 98WO-US19478.
 XX
 PR 26-SEP-1997; 97US-0060172.
 PR 18-SEP-1997; 97US-0059283.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Ayyavoo V, Nagashunmugam T, Weiner DB;
 XX
 DR WPI; 1999-263380/22.
 DR N-PSDB; AAX35225.
 XX
 PT New attenuated vif (viral infectivity factor) genes, used in genetic
 PT vaccines against HIV-1
 XX
 PS Claim 2; Fig 7C; 92pp; English.
 XX
 CC The specification describes novel vif proteins (AAY01969-88) and
 CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
 CC for HIV-1 that has low functional mutagenicity and is conserved. In
 CC addition, attenuated, non functional vif clones are able to induce
 CC immune responses capable of destroying native pathogen. Vif nucleic
 CC acids may be used to immunize mammals. The attenuated, non-functional
 CC vif genes may be used in concert with other HIV-1 genes to produce
 CC vaccine that has a broad immune response against all viral
 CC components, and which mimics many aspects of the immune responses
 CC induced by a live attenuated virus. Prophylactic vaccines which include
 CC vif could limit both viral escape and contribute to lowering the viral
 CC set point during early infection stages.
 XX
 SQ Sequence 192 AA;
 Query Match 10.9%; Score 77; DB 20; Length 192;
 Best Local Similarity 29.9%; Pred. No. 4;
 Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
 QY 22 FDMREALLRVKSSERLAMLRLAGMCHRVLP-----GTGAS-----AIAATVTPKG 69
 Db 112 FDCFSESAR-----KAILGHRVSPRCEYRAGHSKVGSLQYLAIALITPK- 157
 QY 70 ASMKLKPPRQSTKSPLELSRKIREMNTISQESARVNHRLPEGH 116
 Db 158 ---KIKPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192
 RESULT 20
 AAY01978
 ID AAY01978 standard; Protein; 192 AA.
 XX
 AC AAY01978;
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE HIV-1 viral infectivity factor protein N30.
 XX
 KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
 KW viral infectivity factor; HIV-1; vaccine.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9913896-A1.
 XX
 PD 25-MAR-1999.
 XX

PF 18-SEP-1998; 98WO-US19478.
XX
PR 26-SEP-1997; 97US-0060172.
PR 18-SEP-1997; 97US-0059283.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Ayyavoo V, Nagashunmugam T, Weiner DB;
XX
DR WPI; 1999-263380/22.
DR N-PSDB; AAX35226.
XX
PT New attenuated vif (viral infectivity factor) genes, used in genetic
PT vaccines against HIV-1
XX
PS Claim 2; Fig 7C; 92pp; English.
XX
CC The specification describes novel vif proteins (AAY01969-88) and
CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC for HIV-1 that has low functional mutagenicity and is conserved. In
CC addition, attenuated, non functional vif clones are able to induce
CC immune responses capable of destroying native pathogen. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include
CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.
XX
SQ Sequence 192 AA;
XX
Query Match 10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 4;
Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
2y 22 FDVVRALLRVKSSERLALMGCHRVLP---GTGAS-----AIAATVTPKG 69
Db 112 FDCFSERAI-----KAILGHRVSPRCEYRAGHSKVSQYLALALITPK- 157
2y 70 ASMKLKPPRPOSTKSPELRELSRKIRENMKTISQESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192
RESULT 21
AAY01970
ID AAY01970 standard; Protein; 192 AA.
XX
AC AAY01970;
XX
DT 02-JUL-1999 (first entry)
XX
DE HIV-1 viral infectivity factor protein N15.
XX
KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
KW viral infectivity factor; HIV-1; vaccine.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9913896-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US19478.
XX
PR 26-SEP-1997; 97US-0060172.
PR 18-SEP-1997; 97US-0059283.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Ayyavoo V, Nagashunmugam T, Weiner DB;
XX
DR WPI; 1999-263380/22.
DR N-PSDB; AAX35219.
XX
PT New attenuated vif (viral infectivity factor) genes, used in genetic
PT vaccines against HIV-1
XX
PS Claim 2; Fig 7A; 92pp; English.
XX
CC The specification describes novel vif proteins (AAY01969-88) and

DR WPI; 1999-263380/22.
DR N-PSDB; AAX35218.
XX
PT New attenuated vif (viral infectivity factor) genes, used in genetic
PT vaccines against HIV-1
XX
PS Claim 2; Fig 7A; 92pp; English.
XX
CC The specification describes novel vif proteins (AAY01969-88) and
CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC for HIV-1 that has low functional mutagenicity and is conserved. In
CC addition, attenuated, non functional vif clones are able to induce
CC immune responses capable of destroying native pathogen. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include
CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.
XX
SQ Sequence 192 AA;
XX
Query Match 10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 4;
Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
QY 22 FDMREALLRVKSSERLALMGCHRVLP---GTGAS-----AIAATVTPKG 69
Db 112 FDCFSERAI-----KAILGHRVSPRCEYRAGHSKVSQYLALALITPK- 157
QY 70 ASMKLKPPRPOSTKSPELRELSRKIRENMKTISQESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192
RESULT 22
AAY01971
ID AAY01971 standard; Protein; 192 AA.
XX
AC AAY01971;
XX
DT 02-JUL-1999 (first entry)
XX
DE HIV-1 viral infectivity factor protein N17.
XX
KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
KW viral infectivity factor; HIV-1; vaccine.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9913896-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US19478.
XX
PR 26-SEP-1997; 97US-0060172.
PR 18-SEP-1997; 97US-0059283.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Ayyavoo V, Nagashunmugam T, Weiner DB;
XX
DR WPI; 1999-263380/22.
DR N-PSDB; AAX35219.
XX
PT New attenuated vif (viral infectivity factor) genes, used in genetic
PT vaccines against HIV-1
XX
PS Claim 2; Fig 7A; 92pp; English.
XX
CC The specification describes novel vif proteins (AAY01969-88) and

CC the genes encoding them (AA35217-36). The vif gene is an accessory gene
 CC for HIV-1 that has low functional mutagenicity and is conserved. In
 CC addition, attenuated, non functional vif clones are able to induce
 CC immune responses capable of destroying native pathogen. Vif nucleic
 CC acids may be used to immunize mammals. The attenuated, non-functional
 CC vif genes may be used in concert with other HIV-1 genes to produce
 CC vaccine that has a broad immune response against all viral
 CC components, and which mimics many aspects of the immune responses
 CC induced by a live attenuated virus. Prophylactic vaccines which include
 CC vif could limit both viral escape and contribute to lowering the viral
 CC set point during early infection stages.

XX Sequence 192 AA;
 Query Match 10.9%; Score 77; DB 20; Length 192;
 Best Local Similarity 29.9%; Pred. No. 4;
 Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
 QY 22 FDMREALLRVKSSERLAMLALAGMCGHRVLP-----GTGAS-----AIAATVTPKG 69
 Db 112 FDCFSESAIR-----KAILGHRVSPRCEYRAGHSKVSLOYLAIALITPK- 157
 QY 70 ASMKLPPRPOSTKSPELRELSRKIREMKNKTIQSARVNHRLPEGH 116
 Db 158 ---KIRPPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 23
 AAY01972
 ID AAY01972 standard; Protein; 192 AA.
 XX AAY01972;
 AC AAY01972;
 DT 02-JUL-1999 (first entry)
 DE HIV-1 viral infectivity factor protein N22.
 KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
 KW viral infectivity factor; HIV-1; vaccine.

OS Human immunodeficiency virus type 1.
 XX WO9913896-A1.
 PD 25-MAR-1999.
 PF 18-SEP-1999; 98WO-US19478.
 PR 26-SEP-1997; 97US-0060172.
 PR 18-SEP-1997; 97US-0059283.
 PA (UYPE-) UNIV PENNSYLVANIA.
 PI Ayyavoo V, Nagashumugam T, Weiner DB;
 XX WPI; 1999-263380/22.
 DR N-PSDB; AAX35220.
 XX New attenuated vif (viral infectivity factor) genes, used in genetic
 PT vaccines against HIV-1
 XX Claim 2; Fig 7B; 92pp; English.

CC The specification describes novel vif proteins (AAY01969-88) and
 CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
 CC for HIV-1 that has low functional mutagenicity and is conserved. In
 CC addition, attenuated, non functional vif clones are able to induce
 CC immune responses capable of destroying native pathogen. Vif nucleic
 CC acids may be used to immunize mammals. The attenuated, non-functional
 CC vif genes may be used in concert with other HIV-1 genes to produce
 CC vaccine that has a broad immune response against all viral
 CC components, and which mimics many aspects of the immune responses
 CC induced by a live attenuated virus. Prophylactic vaccines which include

CC vif could limit both viral escape and contribute to lowering the viral
 CC set point during early infection stages.

XX Sequence 192 AA;
 Query Match 10.9%; Score 77; DB 20; Length 192;
 Best Local Similarity 29.9%; Pred. No. 4;
 Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
 QY 22 FDMREALLRVKSSERLAMLALAGMCGHRVLP-----GTGAS-----AIAATVTPKG 69
 Db 112 FDCFSESAIR-----KAILGHRVSPRCEYRAGHSKVSLOYLAIALITPK- 157
 QY 70 ASMKLPPRPOSTKSPELRELSRKIREMKNKTIQSARVNHRLPEGH 116
 Db 158 ---KIRPPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 24
 AAW89324
 ID AAW89324 standard; Protein; 192 AA.
 XX AAW89324;
 DT 01-JUN-1999 (first entry)
 DE HIV-1 P protein sequence.
 XX Antigenic composition; primate; lentivirus; nef gene; vaccine;
 KW infection; AIDS; HIV-1.
 XX Human immunodeficiency virus type 1.
 OS US5851813-A.
 PN 22-DEC-1998.

XX 27-JAN-1994; 94US-0188583.
 PR 27-JAN-1994; 94US-0188583.
 PR 12-JUL-1990; 90US-0551945.
 PR 09-JUL-1991; 91US-0727494.
 XX (HARD) HARVARD COLLEGE.
 PI Desrosiers RC;
 XX WPI; 1999-080408/07.
 DR N-PSDB; AAW81866.

PT Lentivirus antigenic compositions - containing lentivirus with nef
 PT gene deletion
 XX Disclosure; Fig 2A-R; 93pp; English.

CC The invention relates to an antigenic composition comprising an isolated
 CC primate lentivirus whose genome contains an engineered non-revertible
 CC null mutation in the nef gene, or an infectious DNA clone in a carrier.
 CC The antigenic composition is used in vaccines against infection by the
 CC lentivirus, e.g. AIDS.

XX Sequence 192 AA;
 Query Match 10.9%; Score 77; DB 20; Length 192;
 Best Local Similarity 27.9%; Pred. No. 4;
 Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
 QY 22 FDMREALLRVKSSERLAMLALAG-----MCGHRVLPGTGASATAATVTPKGASM 72
 Db 112 FDCFSESAIR-----KALLGHVSPRCEYRAGHSKVSLOYLAIALITPK- 157
 QY 73 KUKPPRPOSTKSPELRELSRKIREMKNKTIQSARVNHRLPEGH 116

Db 158 KIKPPLPSVTKLTEDR-----WNKPQTKGHRGSHM-NGH 192

RESULT 25

AA85994

ID AAB85994 standard; Protein; 192 AA.

AC AAB85994;

XX

DT 30-NOV-2001 (first entry)

XX

DE Amino acid sequence of HIV-1 isolate BH10 vif protein.

XX

KW HIV-1; gp120; BH10; vaccine; immunization; vif protein.

XX

OS Human immunodeficiency virus type 1.

XX

PN US6269484-B1.

PD

PD 31-JUL-2001.

XX

PF 30-JUL-1998; 98US-0124900.

XX

PR 07-JUN-1995; 95US-0478536.

PR 19-APR-1995; 95WO-EP01481.

XX

PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX

PI Katinger H, Buchacher A, Ernst W, Ballaun C, Purtscher M;

PI Trkola A, Predl R, Schmatz C, Klima A, Steindl F, Muster T;

XX

DR WPI; 2001-556601/62.

DR N-PSDB; AAH76385.

XX

XX New anti-idiotypic antibodies consisting of one or both amino acid sequences corresponding to amino acid positions 79-84 or 326-400 of the processed gp120 of HIV-isolate BH10, useful as vaccine against HIV-1 infections

FS Claim 1; Columns 29-30; 27pp; English.

XX

CC The invention relates to a peptide fragment comprising of amino acid sequences corresponding to sequences within the processed gp120 of HIV-1 isolate BH10 (GenBank accession M15654). The peptides are useful in the detection, prevention and treatment of HIV-1 infections, and in AIDS therapy. The antibodies are especially useful as vaccines for active and passive immunization, or for the detection and/or determination of HIV-1 infected cells and/or HIV-1 viruses. The present sequence represents the amino acid sequence of a vif protein from HIV-1 isolate BH10 (GenBank accession M15654).

XX

SQ Sequence 192 AA;

Query Match 10.9%; Score 77; DB 22; Length 192;

Best Local Similarity 27.9%; Pred. No. 4;

Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

2y 22 FDMREALLRVKSSERLAMLRLALAG-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 157

Db 112 FDCFSDAIR-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 157

2y 73 KKKPPRQSTKSPRLRLSRKIREMKNKTIQSASRVNHLRPEGH 116

Db 158 KIKPPLPSVTKLTEDR-----WNKPQTKGHRGSHM-NGH 192

RESULT 26

AA60421

ID AAP60421 standard; Protein; 203 AA.

AC AAP60421;

XX

DT 25-MAR-2003 (updated)

XX

DT 20-AUG-1991 (first entry)

XX

DE Sequence of LAV virus ORF Q protein.

XX

KW AIDS vaccine; diagnosis; immunoassay; HIV; HTLV-III.

XX

OS Lymphadenopathy virus.

XX

PN WO8602383-A.

XX

PD 24-APR-1986.

XX

PF 18-OCT-1985; 85WO-EP00548.

XX

PR 18-OCT-1984; 84GB-0016013.

PR 16-NOV-1984; 84GB-0029099.

PR 21-JAN-1985; 85GB-0001473.

XX

PA (INSP) INST PASTEUR.

PA (CNRS) CENT NAT RECH SCIENTIF.

XX

PI Montagnier L, Krust B, Chamaret F, Chermann JC, Barresinou F;

PI Alizon M, Sonigo P;

XX

DR WPI; 1986-119166/18.

DR N-PSDB; AAN60365.

XX

XX Purified glycoprotein and peptide(s) - are recognised by sera contg. antibodies against lymphadenopathy virus and useful in detecting AIDS antibodies or in vaccines

XX

PS Disclosure; Fig 4; 75pp; English.

XX

CC The inventors claim a polypeptide which is recognised by sera of human origin contg. antibodies against the virus of lymphadenopathies (LAV) or acquired immune deficiency syndrome (AIDS). Also claimed are various peptides corresp. to the AA sequences deducible from proteins encoded by LAV DNA, defined by CC specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance with a formula given in the specification.

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 203 AA;

Query Match 10.9%; Score 77; DB 7; Length 203;

Best Local Similarity 27.9%; Pred. No. 4.3;

Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLRLALAG-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 168

Db 123 FDCFSDAIR-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 168

QY 73 KKKPPRQSTKSPRLRLSRKIREMKNKTIQSASRVNHLRPEGH 116

Db 169 KIKPPLPSVTKLTEDR-----WNKPQTKGHRGSHM-NGH 203

RESULT 27

AA43868

ID AAR43868 standard; Protein; 203 AA.

XX

AC AAR43868;

XX

DT 25-MAR-2003 (updated)

DT 23-DEC-1993 (first entry)

XX

DE HTLV-III SOR gene product (Clone BH10).

XX

KW Polypeptide; antibodies; HTLV; AIDS; vaccine.

XX

OS Human T-cell lymphotropic virus.

XX EF552850-A1.
PN
XX
PD 28-JUL-1993.
XX
XX 10-OCT-1985; 93EP-0200929.
XX
XX 10-OCT-1984; 84US-0659339.
PR 23-JAN-1985; 85US-0693866.
PR 10-OCT-1985; 85EP-0307260.
XX
XX (CENZ) CENTOCOR INC.
PA
XX Chang NT, Gallo RC, Wong-staal F;
PI WPI; 1993-236543/30.
DR N-PSDB; AAQ45919.
DR
XX Cloning and expression of new HTLV-III DNA - used to obtain
PT polypeptide(s) and antibodies for diagnosis, prevention and
PT treatment of HTLV-III infection, partic. AIDS
XX
XX Disclosure; Figure 3; 31pp; English.
XX
XX A fragment of DNA approximately 200-500 base pairs in length is
CC ligated into a vector and used to transform E.coli. These cells then
CC express a polypeptide which is immunoreactive with HTLV-III-specific
CC antibody. The HTLV-III polypeptides can be used for the production
CC of antibodies, in immunassays for the detection of HTLV-
CC III-specific antibodies and in vaccines for the prevention of AIDS.
CC The antibodies can also be used to detect HTLV-III polypeptides.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 203 AA;
SQ
Query Match 10.9%; Score 77; DB 14; Length 203;
Best Local Similarity 27.9%; Pred. No. 4.3; Mismatches 11; Indels 32; Gaps 5;
Matches 29; Conservative 11; Mismatches 11; Indels 32; Gaps 5;
QY 22 FDMREALRVKSSERLAMLRLALAG-----MCGHRVLPGTGASATAATVTPKGSM 72
Db 123 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQVLAALITPK---- 168
QY 73 KLKPPRQSTKSPBELSRKIREMKNKTIQSASRVNHRLPESH 116
Db 169 KIRPPLPSVTKLTEDR-----WNKPQKTGHRGSHTM-NGH 203
RESULT 28
AAO19388
ID AAO19388 standard; Protein; 203 AA.
XX
AC AAO19388;
XX
DT 10-DEC-2002 (first entry)
XX
DE Lymphadenopathy-associated virus ORF Q protein.
XX
XX Lymphadenopathy-associated virus; LAV; HIV; human immunodeficiency virus;
KW Lymphadenopathy; AIDS; gag; pol; orf Q; env; orf F; anti-HIV; virucide;
KW vaccine.
XX
OS Lymphadenopathy-associated virus.
XX
XX US6440657-B1.
PN
XX 27-AUG-2002.
PD
XX 06-JAN-2000; 2000US-0478492.
PF
XX 16-NOV-1984; 84GE-0028099.
PR

PR 18-OCT-1985; 85CA-0493377.
PR 03-NOV-1992; 92US-0970954.
PR 17-OCT-1986; 86US-0920119.
PR 01-AUG-1989; 89US-0390499.
PR 06-DEC-1990; 90US-0622278.
PR 20-AUG-1991; 91US-0747506.
PR 01-OCT-1993; 93US-0130565.
PR 06-JUN-1995; 95US-0466920.
PR 05-DEC-1993; 83US-0558109.
PR 28-FEB-1985; 85US-0706562.
PR 30-AUG-1985; 85US-0771230.
PR 30-AUG-1985; 85US-0771247.
PR 30-AUG-1985; 85US-0771248.
XX
XX (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
XX
XX Montagnier L, Krust B, Chamaret S, Clavel F, Chermann J;
PI Barre-sinoussi F, Alizon M, Sonigo P, Cole S, Danos O;
PI Wain-Hobson S;
XX
XX WPI; 2002-711525/77.
DR N-PSDB; AAL49920.
XX
XX Novel chemically synthesized Human Immunodeficiency Virus envelope
PT protein, useful in vitro diagnostic method for the detection of the
PT presence or absence of antibodies that bind to antigens of HIV-1
XX retrovirus
XX
XX Disclosure; Fig 3; 31pp; English.
XX
XX The present invention relates to a chemically synthesised env peptide of
CC Human Immunodeficiency Virus (HIV) of less than 150 amino acid residues.
CC Such a peptide is useful in an in vitro diagnostic method for the
CC detection of the presence or absence of antibodies that bind to antigens
CC of HIV-1 retrovirus, by contacting the peptide with a biological fluid
CC for a time and under conditions sufficient for the peptide and antibody
CC in the biological fluid to form a peptide-antibody complex, detecting the
CC formation of the peptide-antibody complex by comparing the formation of
CC peptide-antibody complex formation with a control sample, where the
CC formation of peptide-antibody complex is correlated with the presence of
CC antibodies that bind to antigens of HIV-1 retrovirus in the biological
CC sample. It can also be used for preparation of vaccine compositions
CC against AIDS or related syndromes. The present sequence is the
CC lymphadenopathy-associated virus LAV ORF Q protein. The LAV virus was
XX isolated from a patient with AIDS.
XX
XX Sequence 203 AA;
SQ
Query Match 10.9%; Score 77; DB 23; Length 203;
Best Local Similarity 27.9%; Pred. No. 4.3; Mismatches 11; Indels 32; Gaps 5;
Matches 29; Conservative 11; Mismatches 11; Indels 32; Gaps 5;
QY 22 FDMREALRVKSSERLAMLRLALAG-----MCGHRVLPGTGASATAATVTPKGSM 72
Db 123 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQVLAALITPK---- 168
QY 73 KLKPPRQSTKSPBELSRKIREMKNKTIQSASRVNHRLPESH 116
Db 169 KIRPPLPSVTKLTEDR-----WNKPQKTGHRGSHTM-NGH 203
RESULT 29
AAB63854
ID AAB63854 standard; Protein; 214 AA.
XX
XX AAB63854;
AC AAB63854;
XX
XX 26-MAR-2001 (first entry)
DT
XX Human prostate cancer associated antigen protein sequence SEQ ID NO:1216.
DE
XX Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW

KW cancer associated antigen; cytostatic; cancer vaccine.
XX Homo sapiens.
OS
XX WO200073801-A2.
XX
XX PD 07-DEC-2000.
XX
XX PF 26-MAY-2000; 2000WO-US14749.
XX
XX PR 28-MAY-1999; 99US-0136526.
XX PR 10-SEP-1999; 99US-0153454.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Obata Y;
XX
XX DR WPI; 2001-025274/03.
XX
XX PT Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer -
XX
XX PS Example 1; Page 747-748; 799pp; English.
XX
XX CC AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.
XX
XX SQ Sequence 214 AA;
Query Match 10.8%; Score 76.5; DB 22; Length 214;
Best Local Similarity 26.1%; Pred. No. 5.2;
Matches 36; Conservative 17; Mismatches 44; Indels 41; Gaps 6;
QY 20 ETDFVMEALLRVKSSERLAVLRA-----LAGMCGHVRVLPQTG-----ASAIA 62
DB 30 EQLDAINKKEIRLIQEEKESTELRAEETENRVASVSLGLENLARVHPGTGTSATVASSLA 89
QY 63 ATVTPKGASM-KLKPPRPQ-----STKSPELRELSRKI-----RENNKTIISOESA 106
DB 90 SSSPPSGHSTFKLTPRSPAREMDRMGVMTLPDSXKXRRKIYAVVEEDGREDKATIKCETS 149
QY 107 -----RVNHRLEPEGH 116
DB 150 PPPTPRALRMTHLPSSY 167
RESULT 30
ID AAY50122 standard; Protein; 373 AA.
XX
XX AC AAY50122;
XX
XX ST 09-FEB-2000 (first entry)
XX
XX DE Human histone fusion protein HHFP.
XX
XX CW Human histone fusion protein; HHFP; nucleosome; basic; histone; H2A;
CW H1; nonhistone protein; DNA binding; leucine zipper; MH2A;
CW transcription regulation; diagnosis; prevention; treatment;
CW proliferative disorder; cancer; inflammatory disorder; asthma;
CW multiple sclerosis; AIDS.
XX
XX JS Homo sapiens.

XX Key Location/Qualifiers
FH Modified-site 2..4
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 7..10
FT /note= "CAMP/CGMP-dependent protein kinase
FT phosphorylation site"
FT Modified-site 8..11
FT /note= "CAMP/CGMP-dependent protein kinase
FT phosphorylation site"
FT Modified-site 10..12
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 13..15
FT /note= "Thr is O-phosphorylated by protein kinase C"
FT Modified-site 16..18
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 16..18
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 77..79
FT /note= "Thr is O-phosphorylated by protein kinase C"
FT Modified-site 117..120
FT /note= "CAMP/CGMP-dependent protein kinase
FT phosphorylation site"
FT Binding-site 133..161
FT /note= "Highly basic DNA binding region"
FT Modified-site 140..142
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 146..148
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 158..160
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Domain 183..213
FT /note= "Leucine zipper"
FT Modified-site 188..190
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 220..223
FT /note= "Thr is O-phosphorylated by casein kinase II"
FT Modified-site 294..296
FT /note= "Thr is O-phosphorylated by protein kinase C"
FT Modified-site 317..319
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 346..348
FT /note= "Ser is O-phosphorylated by protein kinase C"
XX US981221-A.
XX 09-NOV-1999.
XX 26-MAR-1997; 97US-0824878.
XX 26-MAR-1997; 97US-0824878.
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Goli SK;
XX WPI; 1999-833314/54.
XX N-PSDB; AA232676.
XX Nucleic acids encoding histone fusion proteins useful for the
XX prevention, diagnosis and treatment of disorders associated with cell
XX proliferation and inflammation -
XX Claim 1; Fig 1; 29pp; English.
XX This sequence represents human histone fusion protein HHFP. Nucleic
XX acids encoding HHFP were first identified in a human breast tissue
XX cDNA library and this sequence represents a consensus. HHFP is a
XX naturally occurring protein which contains regions homologous with both
XX histones and nonhistone proteins. The N-terminus of HHFP resemble the
XX full-length human histone H2A, while residues 133-161 are highly basic
XX and have similarity with the C-terminus of histone H1, indicating that
XX HHFP has DNA binding potential. There is a leucine zipper region in the

CC nonhistone region of HHFP (between residues 183 and 213) indicating a
 CC potential transcription-regulating function. HHFP has structural and
 CC functional homology with mH2A, a rat histone-nonhistone fusion protein
 CC identified in rat liver nucleosomes. HHFP and nucleotides encoding it
 CC may be used in the diagnosis, prevention and treatment of disorders
 CC associated with cell proliferation (especially cancers) and inflammation
 CC (e.g. AIDS, asthma and multiple sclerosis). They may also be used to
 CC produce and identify modulators of histone function which may be used to
 CC downregulate histone activity and therefore reduce rates of cell
 CC proliferation and reduce inflammatory reactions.
 XX
 SQ Sequence 373 AA;
 Query Match 10.8%; Score 76.5; DB 20; Length 373;
 Best Local Similarity 23.3%; Pred. No. 11;
 Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
 QY 26 REALLRVKSSERLAMRLALAGMCHRVLPDTGASAIATVTPKGASMKLK-PPRPQS 81
 DB 79 RHILLAVANDEELNQLKGVTIASGGVLPNIHPELLA---KRGSGKLEAITTPPPAKK 135
 QY 82 TKSPE-----LRELSRKIREMKNKTISOESARVNHRLPEGHPLLEKRAEYFR 127
 DB 136 AKSPSQKPVSKAGGKKGARKKKQGEVSKAASADSNRGEHLPDGTVLSTKSLFLG 195
 QY 128 HLRSLSQGVNRL 140
 DB 196 QKLNLIHSEISNL 208
 RESULT 31
 AAB30626
 ID AAB30626 standard; Protein; 373 AA.
 XX
 AC AAB30626;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Amino acid sequence of a human histone fusion protein (HFP).
 XX
 KW Human; histone fusion protein; HFP; DNA conformational change; leukaemia;
 KW Incyte clone 2297753; cell proliferation disorder; sarcoma; lymphoma;
 KW cancer; inflammation; allergy; asthma; bronchitis; lupus erythematosus;
 KW multiple sclerosis; thyroiditis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2..4
 FT Modified-site /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 7..10
 FT Modified-site /note= "potential CAMP- and cGMP-dependent protein
 FT Modified-site kinase phosphorylation site"
 FT Modified-site 8..11
 FT Modified-site /note= "potential CAMP- and cGMP-dependent protein
 FT Modified-site kinase phosphorylation site"
 FT Modified-site 10..12
 FT Modified-site /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 13..15
 FT Modified-site /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 16..18
 FT Modified-site /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 77..79
 FT Modified-site /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 117..120
 FT Modified-site /note= "potential CAMP- and cGMP-dependent protein
 FT Modified-site kinase phosphorylation site"
 FT Modified-site 140..142
 FT Modified-site /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 146..148
 FT Modified-site /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 158..160
 FT Modified-site /note= "potential protein kinase C phosphorylation site"

FT Region 183..213
 FT /note= "leucine zipper region"
 FT Modified-site 188..190
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 220..223
 FT /note= "potential casein kinase phosphorylation site"
 FT Modified-site 294..296
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 317..319
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 346..348
 FT /note= "potential protein kinase C phosphorylation site"
 XX
 PN US6136314-A.
 XX
 PD 24-OCT-2000.
 XX
 PF 14-JUL-1999; 99US-0353688.
 XX
 PR 26-MAR-1997; 97US-0824878.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Goli SK;
 XX
 DR WPI; 2001-023156/03.
 DR N-PSDB; RAC62360.
 XX
 PT Novel human histone fusion protein, useful for diagnosing, preventing
 PT or treating disorders associated with cell proliferation (e.g. bone
 PT cancer or leukaemia) or inflammation (e.g. bronchitis or thyroiditis)
 XX
 PS Claim 1; Fig 1A-E; 29pp; English.
 XX
 CC The present sequence represents a human histone fusion protein (HFP).
 CC The protein regulates the conformational changes of DNA. HFP nucleic
 CC acids were first identified in incyte clone 2297753 from a breast
 CC tissue cDNA library. HFP is useful for diagnosing, preventing or
 CC treating disorders associated with cell proliferation (e.g. sarcoma,
 CC lymphoma, leukaemia, or bone, colon or brain cancer) and inflammation
 CC (e.g. allergies, asthma, bronchitis, lupus erythematosus, multiple
 CC sclerosis or thyroiditis).
 XX
 SQ Sequence 373 AA;
 Query Match 10.8%; Score 76.5; DB 22; Length 373;
 Best Local Similarity 23.3%; Pred. No. 11;
 Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
 QY 26 REALLRVKSSERLAMRLALAGMCHRVLPDTGASAIATVTPKGASMKLK-PPRPQS 81
 DB 79 RHILLAVANDEELNQLKGVTIASGGVLPNIHPELLA---KRGSGKLEAITTPPPAKK 135
 QY 82 TKSPE-----LRELSRKIREMKNKTISOESARVNHRLPEGHPLLEKRAEYFR 127
 DB 136 AKSPSQKPVSKAGGKKGARKKKQGEVSKAASADSNRGEHLPDGTVLSTKSLFLG 195
 QY 128 HLRSLSQGVNRL 140
 DB 196 QKLNLIHSEISNL 208
 RESULT 32
 AAM79480
 ID AAM79480 standard; Protein; 1778 AA.
 XX
 AC AAM79480;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3126.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 XX WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001WO-US04098.
 XX PR 03-FEB-2000; 2000US-0496914.
 XX PR 27-APR-2000; 2000US-0560875.
 XX PR 20-JUN-2000; 2000US-0598075.
 XX PR 19-JUL-2000; 2000US-0620325.
 XX PR 01-SEP-2000; 2000US-0654936.
 XX PR 15-SEP-2000; 2000US-0663561.
 XX PR 20-OCT-2000; 2000US-0693325.
 XX PR 30-NOV-2000; 2000US-0728422.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 XX DR N-PSDB; AAK52613.
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 258-259; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX SQ Sequence 1778 AA;
 Query Match 10.8%; Score 76.5; DB 22; Length 1778;
 Best Local Similarity 29.7%; Pred. No. 79;
 Matches 35; Conservative 13; Mismatches 45; Indels 25; Gaps 4;
 QY 3 STSTTTNFAENRPTFGTDFVMDREALLRVKSSERLALMRLAGMCGHRVLPGTGASAI 62
 DB 507 SPRTTENTLERKP-----YSPRDSLPALTSSALAFKLS-----RSKLL 547
 QY 63 ATVTGKASMKLPPRPOSTKSPPELRELSRKIREVNKTISQESARVNHRLPEGHPLLE 120
 DB 548 ATVACLGASPLKVKSKP-SLSWKELRG-----RREVPLAEQVARECERLLEQFPPLFE 599
 RESULT 33
 ID AAM78496
 XX AAM78496 standard; Protein; 2099 AA.
 XX AAM78496;
 AC AAM78496;
 XX 06-NOV-2001 (first entry)
 DT
 XX

DE Human protein SEQ ID NO 1158.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 XX WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001WO-US04098.
 XX PR 03-FEB-2000; 2000US-0496914.
 XX PR 27-APR-2000; 2000US-0560875.
 XX PR 20-JUN-2000; 2000US-0598075.
 XX PR 19-JUL-2000; 2000US-0620325.
 XX PR 01-SEP-2000; 2000US-0654936.
 XX PR 15-SEP-2000; 2000US-0663561.
 XX PR 20-OCT-2000; 2000US-0693325.
 XX PR 30-NOV-2000; 2000US-0728422.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 XX DR N-PSDB; AAK51629.
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 3392-3396; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX SQ Sequence 2099 AA;
 Query Match 10.8%; Score 76.5; DB 22; Length 2099;
 Best Local Similarity 29.7%; Pred. No. 97;
 Matches 35; Conservative 13; Mismatches 45; Indels 25; Gaps 4;
 QY 3 STSTTTNFAENRPTFGTDFVMDREALLRVKSSERLALMRLAGMCGHRVLPGTGASAI 62
 DB 835 SPRTTENTLERKP-----YSPRDSLPALTSSALAFKLS-----RSKLL 875
 QY 63 ATVTGKASMKLPPRPOSTKSPPELRELSRKIREVNKTISQESARVNHRLPEGHPLLE 120
 DB 876 ATVACLGASPLKVKSKP-SLSWKELRG-----RREVPLAEQVARECERLLEQFPPLFE 927
 RESULT 34
 ID AAR43876
 XX AAR43876 standard; Protein; 203 AA.
 XX AAR43876;
 AC AAR43876;

XX 25-MAR-2003 (updated)
 DT 23-DEC-1993 (first entry)
 XX HTLV-III SOR gene product (Clone BH5).
 DE Polypeptide; antibodies; HTLV; AIDS; vaccine.
 KW Human T-cell lymphotropic virus.
 OS EP552850-A1.
 PN 28-JUL-1993.
 XX 10-OCT-1985; 93EP-0200929.
 PF 10-OCT-1984; 84US-0659339.
 PR 23-JAN-1985; 85US-0693866.
 PR 10-OCT-1985; 85EP-0307260.
 XX (CENZ) CENTOCOR INC.
 PA Chang NT, Gallo RC, Wong-staal F;
 PI WPI; 1993-236543/30.
 DR N-PSDB; AAQ45921.
 XX Cloning and expression of new HTLV-III DNA - used to obtain
 PT polypeptide(s) and antibodies for diagnosis, prevention and
 PT treatment of HTLV-III infection, partic. AIDS
 XX Disclosure; Figure 3; 31pp; English.
 PS A fragment of DNA approximately 200-500 base pairs in length is
 CC ligated into a vector and used to transform E.coli. These cells then
 CC express a polypeptide which is immunoreactive with HTLV-III-specific
 CC antibody. The HTLV-III polypeptides can be used for the production
 CC of antibodies in immunoassays for the detection of HTLV-
 CC III-specific antibodies and in vaccines for the prevention of AIDS.
 CC The antibodies can also be used to detect HTLV-III polypeptides.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 203 AA;
 SQ
 Query Match 10.7%; Score 76; DB 14; Length 203;
 Best Local Similarity 27.9%; Pred. No. 5.5;
 Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
 QY 22 FDMREALLRVKSSERLALAG-----KALLGHVSPRCEYQAGHNKVGSLQYLALALITPK---- 168
 Db 123 FDCFSDAIR-----KALLGHVSPRCEYQAGHNKVGSLQYLALALITPK---- 168
 QY 73 KUKPRPOSTKSPRLSRKIRENNKTIQESARVNHRLPEGH 116
 Db 169 KVKPPLPSVTKLTEDR-----WNKPQKTKGHRGSHTM-NGH 203
 RESULT 35
 AAB63752
 ID AAB63752 standard; Protein; 259 AA.
 AC AAB63752;
 XX 26-MAR-2001 (first entry)
 DT Human prostate cancer associated antigen protein sequence SEQ ID NO:1114.
 DE Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
 KW cancer associated antigen; cytostatic; cancer vaccine.
 XX Homo sapiens.
 OS

XX WO200073801-A2.
 PN 07-DEC-2000.
 PD 26-MAY-2000; 2000WO-US14749.
 PF 28-MAY-1999; 99US-0136526.
 PR 10-SEP-1999; 99US-0153454.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Obata Y;
 PI WPI; 2001-025274/03.
 DR Nucleic acids encoding breast, gastric and prostate cancer associated
 PT antigen precursors, useful for diagnosing and treating a condition
 PT characterized by expression of an abnormal amount of a protein, e.g.
 PT cancer -
 XX Example 1; Page 701; 799pp; English.
 PS AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
 CC represent nucleotide sequences encoding human breast, gastric and
 CC prostate cancer associated antigen precursors (CAAP) respectively.
 CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
 CC represent human breast, gastric and prostate CAAP protein sequence
 CC respectively. CAAPs have cytostatic activity and can be used in the
 CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
 CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
 CC condition characterised by expression of an abnormal amount of a protein,
 CC e.g. cancer.
 XX Sequence 259 AA;
 SQ
 Query Match 10.7%; Score 76; DB 22; Length 259;
 Best Local Similarity 20.9%; Pred. No. 7.5;
 Matches 31; Conservative 27; Mismatches 76; Indels 14; Gaps 2;
 QY 4 TSTTTFVARNRPFEGTDFDVMREALLRVKSSERLALAGMCHGRVLPGTGASAI 63
 Db 2 TQFTQYWAQREADFKEITLQERE-ILENAERRLAIFDVLGKCTREBAKXDKATKV 60
 QY 64 TVTFKASMKLKPFPQSTKSPRLSRKIRENNKTIQESARV-----NH 110
 Db 61 ETBEATACLELKNQIKALAKTKGELIKTELKRENESSLIOELTSNKKIITNQ 120
 QY 111 RLPEGHPLLEKRAEYFRHLRLSLKSGQVN 138
 Db 121 RIKELINIIDQKEDTINEFONLASHMEN 148
 RESULT 36
 ABB68120
 ID ABB68120 standard; Protein; 442 AA.
 XX ABB68120;
 AC ABB68120;
 XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 31152.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX Drosophila melanogaster.
 OS WO200171042-A2.
 PN 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 PF

```

23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
(PEKE ) PE CORP NY.
Venter JC, Adams M, Li FWD, Myers EW;
WPI. 2001-656860/75.
N-PSDB; ABL1223.
New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -
Disclosure; SEQ ID NO 31152; 21pp + Sequence Listing; English.
The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
sequences (ABU01840-ABU16175) and the encoded proteins
(ABU57737-ABU72072).
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
Sequence 442 AA;
Query Match 10.7%; Score 75.5; DB 22; Length 442;
Best Local Similarity 21.6%; Pred. No. 17;
Matches 33; Conservative 21; Mismatches 42; Indels 57; Gaps 6
Y 34 SSERLAMRLAGMCG-----HRVLPQTGA-----SAIAATV 65
b 287 SNOEPATPTSLAGSCGVNYIVLDQPRSPVGPAGSKAINGFGSLSLISTPAAVTPV 346
Y 66 TPKGASMKLPPRPQSTKSPELRELS-----RKIRE-----YMKT 100
b 347 TPEAGTILDVPPPPMQTQS--LNSISADTGDTQAKKVTCSTGQYGTIDFRTVALNKS 404
Y 101 ISQESARNHRLPEGHPLLEKRAEYFRHLRSLK 133
b 405 STELPETVTRQSHSHDAEELRIT--RHAKCIR 435
RESULT 37
BG19829
D ABG19829 standard; Protein; 542 AA.
X ABG19829;
X
T 13-FEB-2002 (first entry)
X Novel human diagnostic protein #19820.
X Human; chromosome mapping; gene mapping; gene therapy; forensic;
X food supplement; medical imaging; diagnostic; genetic disorder.
X Homo sapiens.
X
N WO200175067-A2.
X
N 11-OCT-2001.
X
D 30-MAR-2001; 2001WO-US08631.
X
X 31-MAR-2000; 2000US-0540217.
X
R 23-AUG-2000; 2000US-0649167.
X
A (HYSE-) HYSEO INC.

```

```
XX Dmanac RT, Liu C, Tang YT;
PI WFI; 2001-639362/73.
CC N-PSDB; AAS84016.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX Claim 20; SEQ ID No 50188, 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC centromere mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 542 AA;
SQ
Query Match 10.7%; Score 75.5; DB 22; Length 542;
Best Local Similarity 23.7%; Pred.No.22;
Matches 31; Conservative 18; Mismatches 53; Indels 29; Gaps 4;
QY 9 NFVAENRPTFGTDFVMREALLRVKSSERLAMLRLALAGMCGHRVLPQTGASAIAATVT-- 66
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
235 NULLILKKPVF-----LKPKRLLLHLRPSLECCCPMWIKGASMSRDIAKTPL 281
QY 67 --PKGASMKLKP RPPOSTKSPELRSLRKIREMNKTISQESARVNHRLPGHHLEKR-- 122
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
282 PGRASADLMFPKGGSLEAEUQLKNLSIQSTQAIDEHLXR-----LFERRVK 331
QY 123 AEVFRLRSGLK 133
Db : | | : | | : | | : | | : | | : | | : | | : | | : |
332 AEWVTNQBELK 342
RESULT 38
ABJ19818
ID ABJ19818 standard; Protein; 1257 AA.
AC ABJ19818;
DT 10-APR-2003 (first entry)
DE XX Androgen-independent prostate cancer-related protein - SEQ ID NO 51.
EX DE Androgen-independent cancer; androgen ablation therapy; prostate cancer;
KW KW Androgen-dependent prostate cancer; prostate cancer.
OS OS Unidentified.
XX OS
FN FN WO200298358-A2.
PD PD 12-DEC-2002.
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[illegible]

PI Venter JC, Adams M, Li FWD, Myers EW;
XX WI; 2001-656860/75.
DR N-PSDB; ABL12700.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -
XX
XX Disclosure; SEQ ID NO 32583; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins
(ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1116 AA;
30
Query Match 10.5%; Score 74.5; DB 22; Length 1116;
Best Local Similarity 29.2%; Pred. No. 71;
Matches 49; Conservative 19; Mismatches 55; Indels 45; Gaps 10;
2y 1 MESTSTTNFVAENRPTFGETFDVNRALLRVKSSERLALMRLAGMCGHRVLPGTGASA 60
3b 747 MASTSTS-----RQSPCPAT---PRAGLSRKNSCSTFSVNLGLAGMLNERGIKAVTPSA 797
2y 61 I-----AATVTPKGASKLKP RPQSTKSPELRELS-----RKI-----REMKN 99
3b 798 LNTPAGEFNPSTVTTCN-SPGSPFPAQSP-PLFGLLSCGADLIRKIVGDQHQOQOQK 855
2y 100 TISOESARVNRHLEPGHPLLEKRAEYFRHLRSL-----XSQGVNRLI 141
3b 856 QRSLSKQOQOQKIMLSH--LERRA-----LRSLNLIEKVESIGLENII 896

Search completed: November 14, 2003, 10:40:16
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:35 ; Search time 21 seconds

(without alignments)
284.087 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 708

Sequence: 1 MESTSTTTFVFAENRPTFGE.....RAEYFRHLRLSKSQGVNRLI 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pdp.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81.5	11.5	1419	4	US-09-252-991A-31822
2	80	11.3	473	4	US-09-252-991A-31406
3	78	11.0	686	4	US-09-107-532A-5002
4	77	10.9	192	3	US-09-124-900-4
5	77	10.9	203	3	US-08-463-210-10
6	76.5	10.8	373	2	US-08-824-878-1
7	76.5	10.8	373	3	US-09-353-688-1
8	76.5	10.8	501	4	US-09-252-991A-23033
9	75.5	10.7	741	4	US-09-252-991A-30333
10	74	10.5	231	4	US-09-252-991A-32190
11	74	10.5	383	4	US-09-252-991A-27087
12	72.5	10.2	248	4	US-09-252-991A-32808
13	72.5	10.2	342	3	US-08-911-853-2
14	72.5	10.2	342	3	US-09-479-409-2
15	72.5	10.1	282	4	US-09-479-453-2
16	71.5	10.1	282	4	US-09-252-991A-26169
17	71.5	10.1	976	3	US-08-894-997-50
18	71.5	10.1	2293	3	US-09-369-590-2
19	71	10.0	558	4	US-09-252-991A-26115
20	70.5	10.0	329	4	US-09-252-991A-30436
21	70.5	10.0	954	3	US-09-251-645-12
22	70	9.9	185	4	US-09-252-991A-24804
23	70	9.9	242	4	US-09-252-991A-19038
24	70	9.9	443	2	US-08-793-475-6
25	69.5	9.8	296	4	US-09-252-991A-23961
26	69.5	9.8	354	2	US-08-216-894-4
27	69.5	9.8	354	3	US-09-115-746-4

28	69.5	9.8	564	2	US-08-216-894-2	Sequence 2, Appli
29	69.5	9.8	564	3	US-09-115-746-2	Sequence 2, Appli
30	69.5	9.8	643	2	US-08-216-894-8	Sequence 8, Appli
31	69.5	9.8	643	3	US-09-115-746-8	Sequence 8, Appli
32	69.5	9.8	671	4	US-09-252-991A-19375	Sequence 19375, A
33	69	9.7	232	4	US-09-252-991A-30831	Sequence 30831, A
34	69	9.7	411	4	US-09-252-991A-25526	Sequence 25526, A
35	69	9.7	454	4	US-09-252-991A-24836	Sequence 24836, A
36	69	9.7	461	4	US-09-252-991A-32102	Sequence 32102, A
37	69	9.7	553	3	US-09-413-814-3	Sequence 3, Appli
38	69	9.7	834	1	US-07-977-434-8	Sequence 8, Appli
39	69	9.7	834	1	US-08-458-819-8	Sequence 8, Appli
40	69	9.7	834	5	FCT-US91-07035-8	Sequence 8, Appli
41	69	9.7	1064	4	US-09-252-991A-17508	Sequence 17508, A
42	68.5	9.7	371	4	US-09-252-991A-32348	Sequence 32348, A
43	68.5	9.7	408	4	US-09-252-991A-21775	Sequence 21775, A
44	68.5	9.7	600	4	US-09-134-001C-5293	Sequence 5293, Ap
45	68	9.6	155	4	US-09-252-991A-18135	Sequence 18135, A

ALIGNMENTS

RESULT 1
US-09-252-991A-31822
; Sequence 31822, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31822
; LENGTH: 1419
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31822

Query Match 11.5%; Score 81.5; DB 4; Length 1419;
Best Local Similarity 28.5%; Pred. No. 3.7;
Matches 35; Conservative 16; Mismatches 59; Indels 13; Gaps 5;
QY 25 MREALLRVKSSER-LA-----MLRALAGMCHRYLPCTGASATAATVTPKGASMKLKP RP 79
Db 881 LREQLLRARELDQLADTGELEALLAGLAGRFVAFPGGDPINPQVPSGRNLF AF----- 936
QY 80 QSTKSPSELRLSKITREMNKTSQESARVNH--RLPEGHPLLEKRAEYFRHLRLSKSQGV 137
Db 937 EADKVPTRAAEAGAEAFQQLL--ESYRAEHQGRAPEKLAFLSWSETMRHLGIVESQAL 994
QY 138 NRL 140
Db 995 HAL 997

RESULT 2
US-09-252-991A-31406
; Sequence 31406, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18


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; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,210
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/693,866
; FILING DATE: 23-JAN-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/559,339
; FILING DATE: 10-OCT-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Serunian, Leslie A.
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4193US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: HTLV-III
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..203
; OTHER INFORMATION: /note= "sor protein of HTLV-III"
;
; JS-08-463-210-10

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Query Match 10.9%; Score 77; DB 3; Length 203;
Best Local Similarity 27.9%; Pred. No. 0.82;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

2y 22 FDVNRALLRVKSSERLAMLALAG-----MCHRVLPGTGASAIATVTPKGASM 72
; Sequence 1, Application US/08824878
; Patent No. 5981221
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HISTONE FUSION PROT
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/353,688
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/824,878
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

```

```

; JS-08-824-878-1
; Sequence 1, Application US/08824878
; Patent No. 5981221
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HISTONE FUSION PROT
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,878
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0255 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT05
; CLONE: 2297753
;
; US-08-824-878-1
;
; Query Match 10.8%; Score 76.5; DB 2; Length 373;
; Best Local Similarity 23.3%; Pred. No. 2.2;
; Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
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; QY 26 REALLRVKSSERLAMLALAGMCHRVLPGTGASAIATVTPKGSMKLGK----PPRPOS 81
; DB 79 RHILLAVANDEELNQLKGVTIASGGVLPNIHPPELLA---KRGSGKLEAIIITPPAKK 135
; QY 82 TKSP-----LRELSRKIREMKNKTIQESARVNHRLPEGHPLLEKAEYFR 127
; DB 136 AKSPQKQPVSKAGKKGARKKKQGEVSKAAGSNNRGEHLDPDFTVLTSLFLG 195
; QY 128 HLRSLSQGVNRL 140
; DB 196 QKLNLIHSEISNL 208
;
; RESULT 7
; US-09-353-688-1
; Sequence 1, Application US/09353688
; Patent No. 6136314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HISTONE FUSION PROT
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/353,688
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/824,878
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0255 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT05
CLONE: 2297753
US-09-353-688-1

Query Match 10.8%; Score 76.5; DB 3; Length 373;
Best Local Similarity 23.3%; Pred. No. 2.2;
Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;

QY 26 REALLRVKSSERLAMLALAGMCGHRVLPGTGASAIATVTPKGASMKLK-----PPRFQS 81
DB 79 RHILLAVANDEELNQLKGVTIASGVLPNIHPELLA---KRGSKGKLEAIITPPPAKK 135
QY 82 TKSPE-----LRELSRKIRENMKTISOESARVNHRLPEGHPLLEKRAEYFR 127
DB 136 AKSPQKPVSKKAGGKKGARKSKKQGEVSKAASDAUNNREGHLPDGVTLSTKSLFLG 195
QY 128 HLRLSKSQGVNRL 140
DB 196 QKLNLIHSEISNL 208

RESULT 8
US-09-252-991A-23033
; Sequence 23033, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23033
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23033

Query Match 10.8%; Score 76.5; DB 4; Length 501;
Best Local Similarity 23.7%; Pred. No. 3.2;
Matches 27; Conservative 23; Mismatches 45; Indels 19; Gaps 4;

QY 31 RVKSSERLAMLAL-AGMCGHRV---LPGTGASAIATVTPKGASMKLKPPRPOSTKSP 86
DB 91 RVENEDMHADLVIVGAGVMSALALSGLELLV---DGGSLDVAPFKPEAPYEP 146
QY 87 LRELSRKIRENMKTISOESARVNHRLPEGHPLLEKRAEYFRHLRLSKSQGVNRL 140
DB 147 V-----SALSEASRRILQHLAWDGIIVAFRAEPYEMQVWDGSGTGRI 189

RESULT 9
US-09-252-991A-30333
; Sequence 30333, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30333
LENGTH: 741
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30333

Query Match 10.7%; Score 75.5; DB 4; Length 741;
Best Local Similarity 27.9%; Pred. No. 7.2;
Matches 34; Conservative 14; Mismatches 41; Indels 33; Gaps 6;

QY 25 MREALLRVKSSERLAML-ALAGMCGHRVLP-----TGASAIATVTPKGASMKLKPP 77
DB 39 LRDAL---GTHRRARRDGLAGGQHPRPFGDQHLRTGAAA-AGAAARPAGDRPFLDRP 93
QY 78 RPOSTKSP-----LRELSRKIRENMKTISOESARVNHRLPEGHPLLEKRAEYFRH 128
DB 94 RPSRQDLPEPAGDQGRRLGTVPRRRRLRTAAE-----HGLCRRRGQHLRL 141
QY 129 LR 130
DB 142 LR 143

RESULT 10
US-09-252-991A-32190
; Sequence 32190, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32190
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32190

Query Match 10.5%; Score 74; DB 4; Length 231;
Best Local Similarity 27.8%; Pred. No. 2.1;
Matches 27; Conservative 14; Mismatches 40; Indels 16; Gaps 3;

QY 51 RVLPGT-----GASAIATVTPKGASMKLKPPRPOSTKSPBLRELSRKIRENMKTISO 104
DB 88 RVTPGTLSGKPPASSAMRATLRLSSPAW-LAQFRNTSSNADQSTPGLRSTRAFSGTAARS 146
QY 105 SARVNHRLPEGHPLLEKRAEYFRHLRLSKSQGVNRL 141
DB 147 SARTAERLPPKRI-----GVRTASQMTSRLI 174

RESULT 11
US-09-252-991A-27087
; Sequence 27087, Application US/09252991A
; Patent No. 6551795

```
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; NUMBER OF SEQUENCES: 37
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27087
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27087

Query Match 10.5%; Score 74; DB 4; Length 383;
Best Local Similarity 29.4%; Pred. No. 4.3;
Matches 32; Conservative 9; Mismatches 42; Indels 26; Gaps 5;

QY 30 LRVKSSERLMLR-----ALAGWCHRVLPGTGASAIATVTPKGSMK-----LKPP 77
Db 139 LRAAQRIPRLRLRGAGGAGGAGGALFGAAGVGVHVPQGHGAADRELPGDLQPP 198
QY 78 ----RPOSTKSPELRSKIRENMKTIQSASR-----VNHRLPEG 115
Db 199 ARRTPGAGGGRILRL---PAFRTAGSELASRPVYPHLLNQRLPAG 244

RESULT 12
US-09-252-991A-32808
; Sequence 32808, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; NUMBER OF SEQUENCES: 37
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32808
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32808

Query Match 10.2%; Score 72.5; DB 4; Length 248;
Best Local Similarity 29.6%; Pred. No. 3.4;
Matches 32; Conservative 10; Mismatches 41; Indels 25; Gaps 6;

QY 33 KSSERLMLRALAGWCHRVLPGTGASAIATVTPKGSMKLPKPPRQST-----KSP 87
Db 80 RSNLSLCILRRSFC-----ARFCSETACPR--ARPERPFRAPTSDSPAKPFI 128
QY 88 RELSRKIRENMKTIQSASRVNHLRPEGHPLLEKRAE-----YFRHLR 130
Db 129 RPTSMKIHCMRRLDQEVPRSTDCP-GHP---ARAPFAPGVYSPHSR 172

RESULT 13
US-08-911-853-2
; Sequence 2, Application US/08911853
; Patent No. 6048710
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
```

```
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,853
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,092
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-911-853-2

Query Match 10.2%; Score 72.5; DB 3; Length 342;
Best Local Similarity 28.2%; Pred. No. 5.3;
Matches 29; Conservative 16; Mismatches 39; Indels 19; Gaps 4;

QY 24 VMREALLRVKSSERLMLRALAGWCHRVLPGTGASAIATVTPKGSMKLPKPPRQST 82
Db 101 VLEDQLVH---SERLASIGRLAGVAHGNVPTGIACLAQNL-----REERE 145
QY 83 KSPFLRSLKIRENMKTIQSASRVNHLRPEGHPLLEKRAEY 125
Db 146 GDEELGEISNQILDQTKRISR---IVQSLMNFHAHQQQRAEY 185

RESULT 14
US-09-479-409-2
; Sequence 2, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
```

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-479-409-2
;
Query Match
Best Local Similarity 10.2%; Score 72.5; DB 3; Length 342;
Matches 29; Conservative 16; Mismatches 39; Indels 19; Gaps 4;
;
Qy 24 VMREALLRVKSSERLAMLALACMGCHRV-LPTGASATAATVTPKGASMKLKPPRPOST 82
Db 101 VLEDQLVH---SERLASIGRLAAGVAHEIGNVPTGIACLAQNL-----REERE 145
;
Qy 83 KSPFELRSRKIREMNKTIQESARVNHRLPEGHPLLEKRAEY 125
Db 146 GDEELGEISNQILDQTKRISR---IVQSLMNFHAGQQQRAEY 185
;
RESULT 15
US-09-479-453-2
; Sequence 2, Application US/09479453
; Patent No. 6313283
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;

US-09-479-453-2
;
Query Match
Best Local Similarity 10.2%; Score 72.5; DB 4; Length 342;
Matches 29; Conservative 16; Mismatches 39; Indels 19; Gaps 4;
;
Qy 24 VMREALLRVKSSERLAMLALACMGCHRV-LPTGASATAATVTPKGASMKLKPPRPOST 82
Db 101 VLEDQLVH---SERLASIGRLAAGVAHEIGNVPTGIACLAQNL-----REERE 145
;
Qy 83 KSPFELRSRKIREMNKTIQESARVNHRLPEGHPLLEKRAEY 125
Db 146 GDEELGEISNQILDQTKRISR---IVQSLMNFHAGQQQRAEY 185
;
RESULT 16
US-09-252-991A-26169
; Sequence 26169, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26169
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
;
US-09-252-991A-26169
;
Query Match
Best Local Similarity 10.1%; Score 71.5; DB 4; Length 282;
Matches 42; Conservative 10; Mismatches 63; Indels 31; Gaps 7;
;
Qy 14 NRPTFGTTFDVMREALLRVKSSERLAMLR-----ALAGMCGHRVLPOT---GASATAATV 65
Db 138 SRPAPGG-----RSRTLASAPHRSARPRWTPQTRKAGRSGQGLRPGADRCGCGGSAT- 191
;
Qy 66 TPKGASMKLKXPPR-----POSTKSPFELRSRKIREMNKTIQESARVNHRLP 113
Db 192 TPAPRSVPPSPARYPAPVAGDRDRSPAPCPASRRLSRTDRFGNRAPSPAGNREIH--P 249
;
Qy 114 EGHPL---LEKRAEYFRHLRLSKSQ 136
Db 250 ACQPLFRRLHARQAWLDGKTRXHG 275
;
RESULT 17
US-08-894-997-50
; Sequence 50, Application US/08894997A
; Patent No. 6270990
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; APPLICANT: Schoenherr, Christopher J
; TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
; FILE REFERENCE: 17810-502 NRSF
; CURRENT APPLICATION NUMBER: US/08/894,997A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/US96/02817
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/398,590
; EARLIER FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 976
;

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
US-08-894-997-50

Query Match
Best Local Similarity 10.1%; Score 71.5; DB 3; Length 976;
Matches 38; Conservative 20; Mismatches 67; Indels 13; Gaps 6;

Qy 1 MESTTTTNFVAENRPTTGETFDV---MREALLRVKSSERLAMLRLALAGMCGHVRVLPQTG 57
Db 661 IEVAQTAPTQVOEPPVSEPPVRPTKRSSLRKDRAEKLSLLSEMARQ--EQVLMGVG 718
Qy 58 ASAAATVTPKGASMKLKPFRQSTKSP--LRLELSRKIRENMKTIISQESARVNHRLPEG 115
Db 719 LVPVRDSKLLKGNKAQPPAPPS--PSPKGNRSREETPKDQEM---VSDGEGTIVFPLKKG 774
Qy 116 HPLLEKRAEYFRHLRSLK 133
Db 775 GP--EEAGESPAELAAALK 790

RESULT 18
US-09-368-590-2
; Sequence 2, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; EARLIER FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2293
; TYPE: PRT
; ORGANISM: Human
US-09-368-590-2

Query Match
Best Local Similarity 10.1%; Score 71.5; DB 3; Length 2293;
Matches 34; Conservative 17; Mismatches 71; Indels 17; Gaps 5;

Qy 12 AENRPTTGETFDVMEALLRVKSSERLAMLRLALAGMCGHVRVLPQTGASAAIAATVTPKGAS 71
Db 1899 AEVTRTVG---YVQELKPERLQPRIDELPEIPGRVFPALPAAPEDAETPATP--AA 1952
Qy 72 MKLKPFRQSTKSP--LRLELSRKIR--ENKTIISQESARVNHRLPE-----GHPLE 120
Db 1953 ABOVPRPERQESADRAEELPERRRPERQESYDQSEEAARRRRRPERQESAEHAHSLTL 2012
Qy 121 KRAEYFRHLRSLKSGVNR 139
Db 2013 GRYEQMERRRRRRLER 2031

RESULT 19
US-09-252-991A-26115
; Sequence 26115, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26115
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26115

Query Match
Best Local Similarity 10.0%; Score 71; DB 4; Length 558;
Matches 22; Conservative 11; Mismatches 31; Indels 28; Gaps 3;

Qy 55 GTGASAAIAATVTPK-----GASMKLKPFRQSTKSPLELSRKIREMN 98
Db 284 GPAAGAPAGAAQPRLGTAAQRHRRQLREADGRAVRLPADRPEGLPDQ----RRKVRPRP 339
Qy 99 KTISQESARVNH-----LPEGHPLLEKR 122
Db 340 TALGKTADRGHRLQLAVARPLFGGHPAPER 371

RESULT 20
US-09-252-991A-30436
; Sequence 30436, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30436
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30436

Query Match
Best Local Similarity 10.0%; Score 70.5; DB 4; Length 329;
Matches 38; Conservative 14; Mismatches 61; Indels 55; Gaps 6;

Qy 3 STSTTTNFVAENRPTTGETFDVMEALLRVKSSERL-----AMRLALAGM 47
Db 26 TTSSPTSAATRSASASRPVNPCTCSGSSGERTRAAALRRFVAGAGRGALRLGL 85
Qy 48 C-----GHRVLPGTGASAAIAATVTPKGSMKLPFRQSTK-----SP 85
Db 86 CQQRPRGRDGRRRPAGRESFGD-----ALRPVVPVAMSRPPPCATPGAGGAP 138
Qy 86 ELRELSRKIREMN--KTISQESARVNH-----PEGHPLLEKR 122
Db 139 ADRADGRAALALGHAASIGERGAIVRHLALLRPLGAPPPGPANQPR 186

RESULT 21
US-09-251-645-12
; Sequence 12, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:

```



```
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 954
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-12

Query Match          10.0%; Score 70.5; DB 3; Length 954;
Best Local Similarity 23.0%; Pred. No. 37;
Matches 32; Conservative 22; Mismatches 54; Indels 31; Gaps 5;

QY 3 STSTTNFVAEN-----RPTGETFVMEALLRVKSSERLMLRALAGMCGHRVLP 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 SPTNATN-VAIRNRPVAPKPTLPKASTSSQSTTYPIKSA-----IKPT 737

QY 56 TGASAIATVTPKGASMKLKKPRPOSTKSPELRSLRKIREMNKTIISOESAR---VNRH 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 738 TSGSSITAPLSPVGNKSTPEILSPSTQNSSSAISTNLQKSFILYRADNRSPEDMQSK 797

QY 112 LPEGH-----PLEKRAEYF 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 798 FPEGKAWTFLDTQMARQF 816

RESULT 22
US-09-252-991A-24804
; Sequence 24804, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24804
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24804

Query Match          9.9%; Score 70; DB 4; Length 185;
Best Local Similarity 27.8%; Pred. No. 4.4;
Matches 32; Conservative 13; Mismatches 46; Indels 24; Gaps 4;

QY 31 RVKSSERLMLRALAGMCGHRVLPOTGASAIATVTPKGASMKLKKPRPQSTKSPELREL 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 RVRS---MAASRAAA-----SAKAGICATASPSHRRPKALPSARRGSAVSPARRL 86

QY 91 -----SRKIREMNKTIQSASRWHLPEGHPLLEKR---AEYFRLSLKS 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 LTAPALPSAKARDSSCSPPAASRRKRLPSSSRKLTRRAALAAFFLPLSALFS 141

RESULT 23
US-09-252-991A-19038
; Sequence 19038, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19038
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19038

Query Match          9.9%; Score 70; DB 4; Length 242;
Best Local Similarity 27.9%; Pred. No. 6.3; 23; Indels 14; Gaps 2;
Matches 19; Conservative 12; Mismatches 19; Indels 14; Gaps 2;

QY 32 VKSSERLMLRALAGMCGH-----RVLPOTGASAIATVTPKGASMKL-----KPP 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 IRSCEVAAGKSGLCWHSREEDSPCPRIPAVAIAAICATSPRRWTMSLTATARSAG 80

QY 78 RPQSTKSP 85
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 APQAASPP 88

RESULT 24
US-08-795-475-6
; Sequence 6, Application US/08795475
; Patent No. 5983390
; GENERAL INFORMATION:
; APPLICANT: Bjvick, Lars
; APPLICANT: Sjøvring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-475-6
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[illegible]

```

; MOLECULE TYPE: protein
US-09-115-746-4

Query Match
Best Local Similarity 9.8%; Score 69.5; DB 3; Length 354;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPQTGASAIATVTPKGASMKLKPPRPOSTKS-PELREL 90
DB 193 LKSSKYIAW-----PLOGWQATFGGDHPKSDIVPRGSPSQLOQAENNTNSKKEWTKL 247

QY 91 SRKIRE-----MNKTIQSARVNNHRLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
DB 248 REKVKAKEKLDAINRATKLEER-NOAYKAHKAEEKAKTFORLITFESININ 302

RESULT 29
US-09-115-746-2
; Sequence 2, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchoff, Louis V.
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-MAR-1994
; FILING DATE: 24-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-216-894-2

Query Match
Best Local Similarity 9.8%; Score 69.5; DB 2; Length 564;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPQTGASAIATVTPKGASMKLKPPRPOSTKS-PELREL 90
DB 193 LKSSKYIAW-----PLOGWQATFGGDHPKSDIVPRGSPSQLOQAENNTNSKKEWTKL 247

QY 91 SRKIRE-----MNKTIQSARVNNHRLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
DB 248 REKVKAKEKLDAINRATKLEER-NOAYKAHKAEEKAKTFORLITFESININ 302

RESULT 29
US-09-115-746-2
; Sequence 2, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchoff, Louis V.
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-MAR-1994
; FILING DATE: 24-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-216-894-2

Query Match
Best Local Similarity 9.8%; Score 69.5; DB 2; Length 564;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPQTGASAIATVTPKGASMKLKPPRPOSTKS-PELREL 90
DB 193 LKSSKYIAW-----PLOGWQATFGGDHPKSDIVPRGSPSQLOQAENNTNSKKEWTKL 247

QY 91 SRKIRE-----MNKTIQSARVNNHRLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
DB 248 REKVKAKEKLDAINRATKLEER-NOAYKAHKAEEKAKTFORLITFESININ 302

RESULT 29
US-09-115-746-2
; Sequence 2, Application US/09115746
; Patent No. 6228601

```

```

; GENERAL INFORMATION:
; APPLICANT: Kirchoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,894
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-115-746-2

Query Match
Best Local Similarity 9.8%; Score 69.5; DB 3; Length 564;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPQTGASAIATVTPKGASMKLKPPRPOSTKS-PELREL 90
DB 193 LKSSKYIAW-----PLOGWQATFGGDHPKSDIVPRGSPSQLOQAENNTNSKKEWTKL 247

QY 91 SRKIRE-----MNKTIQSARVNNHRLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
DB 248 REKVKAKEKLDAINRATKLEER-NOAYKAHKAEEKAKTFORLITFESININ 302

RESULT 30
US-08-216-894-8
; Sequence 8, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

```

```
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/216,894
/ FILING DATE: 24-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 85326/102/DRLO
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 643 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-216-894-8

Query Match          9.8%; Score 69.5; DB 2; Length 643;
Best Local Similarity 22.4%; Pred. No. 28;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCHRVLPFGTGASAIATVTPKGASMKLKPFPQSTKS-PELREL 90
Db 193 LKSSXYIAW-----PLQGWAATFGGDHPKSDLVPRGSPSQLOQAENNITNSKKEMTKL 247

QY 91 SKKIRE-----MNKTIQESARVNHRLPEGHPLLEKRAEYFRLHLSLKSGQVN 138
Db 248 REKVKAKEKLDAINRATKLEBER-NOAYKAAHKAEBEAKTFORLITFESENIN 302

RESULT 31
US-09-115-746-8
; Sequence 8, Application US/09115746
; Patent No. 6228601
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; TITLE OF INVENTION: WITH TRYPAOSOMA CRUZI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,746
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,894
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 643 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-115-746-8
Query Match          9.8%; Score 69.5; DB 2; Length 643;
Best Local Similarity 22.4%; Pred. No. 28;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCHRVLPFGTGASAIATVTPKGASMKLKPFPQSTKS-PELREL 90
Db 193 LKSSXYIAW-----PLQGWAATFGGDHPKSDLVPRGSPSQLOQAENNITNSKKEMTKL 247

QY 91 SKKIRE-----MNKTIQESARVNHRLPEGHPLLEKRAEYFRLHLSLKSGQVN 138
Db 248 REKVKAKEKLDAINRATKLEBER-NOAYKAAHKAEBEAKTFORLITFESENIN 302

RESULT 32
US-09-252-991A-19375
; Sequence 19375, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19375
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
/
US-09-252-991A-19375

Query Match          9.8%; Score 69.5; DB 4; Length 671;
Best Local Similarity 28.5%; Pred. No. 29;
Matches 41; Conservative 12; Mismatches 56; Indels 35; Gaps 8;

QY 15 RPTFGETFDYMR-----ALLRVKSSERLAMLALAGMCHRVLPFGTGASAIATVTPKGAS 71
Db 455 RP--GETGRVARHPGGAHFR-----RIPRCRPGAPRLGLQFGTGTGTGGAADQE--- 504

QY 72 MKLKPFPQSTKSPLELSR-----KIREMNKTIQESA-----RVNH----- 110
Db 505 RRLRPRPREVR-PRLFRPFRAGGDFRALAVPRLRQRPNDVLHQRHAAPPRQGHLLRM 563

QY 111 RLPEGHPLLEKRAEYFRLHLSLKS 134
Db 564 RFPAGLPALPQRLHRRSRVPRS 587

RESULT 33
US-09-252-991A-30831
; Sequence 30831, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30831
; LENGTH: 232
; TYPE: PRT
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; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30831

Query Match 9.7%; Score 69; DB 4; Length 232;
 Best Local Similarity 25.6%; Pred. No. 7.7;
 Matches .22; Conservative 14; Mismatches 34; Indels 16; Gaps 4;

QY 49 GHRVLPGTGASAIATVTPKASMKLKPQSTKSPEL-----RELRSKIREMNKTI 102
 DB 121 GHRV--AGSRAATARP-----ARPRGSRVAFGIPARSFARVHRRLATLHRQPQ 172
 QY 103 QSARVNHLPEGHPLLEKRAEYFRH 128
 DB 173 PQLRTANGKIP--RPKQTNRSENFLH 196

RESULT 34
 US-09-252-991A-25526
 ; Sequence 25526 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25526
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25526

Query Match 9.7%; Score 69; DB 4; Length 411;
 Best Local Similarity 30.5%; Pred. No. 17;
 Matches 32; Conservative 12; Mismatches 53; Indels 8; Gaps 5;

QY 14 NRPTFGTGVNREALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAI--AATVTPKAS 71
 DB 128 HRPLQSGERLRQLLR--RAPHLQGRAGRAGR--TGGGAAGADRRLRHRQFAP 184
 QY 72 MKLKPQSTKSPELRELSKIREMNKTIQESARVNHLPEGH 116
 DB 185 RSGRRPRGSPHAGRLRRRRHRRH--RQHPPRPAHRQP--GH 226

RESULT 35
 US-09-252-991A-24836
 ; Sequence 24836 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24836
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24836

Query Match 9.7%; Score 69; DB 4; Length 454;
 Best Local Similarity 28.1%; Pred. No. 19;
 Matches 27; Conservative 13; Mismatches 48; Indels 8; Gaps 3;

QY 26 REALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAIATVTPKASMKLKPQSTK 82
 DB 110 RHQLWRLPGDPQPVARGALAGLAGADLPRGLADAAARPRGSORIPQDPQGRQP 169
 QY 83 KSPELRELSKIREMNKTIQESARVNH-----RLP 113
 DB 170 SPAGLRGIPRCAAGGVVROLCAALDHHFFRRLP 205

RESULT 36
 US-09-252-991A-32102
 ; Sequence 32102 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 32102
 ; LENGTH: 461
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-32102

Query Match 9.7%; Score 69; DB 4; Length 451;
 Best Local Similarity 26.8%; Pred. No. 20;
 Matches 30; Conservative 15; Mismatches 57; Indels 10; Gaps 3;

QY 25 MREALLRVKSSERLAMLRLALA-GMCGHRVLPFGTGASAIATVTPKASMKLKPQSTK 83
 DB 309 LRQPAQVAYGQALAEQFVLALGTAGHRAAPAQAQHA-----KGAAGHLHPRHVERQ 361
 QY 84 SPDELRELSKIREMNKTIQESARVNHLPEGHPLLEKRAEYFRHLRLSKSO 135
 DB 362 GMEVEEPFAD--EIADTIQGVRAEHGDFLGAADOVHLRFRPLQVERPQ 411

RESULT 37
 US-09-413-814-3
 ; Sequence 3 Application US/09413814
 ; Patent No. 6225064
 ; GENERAL INFORMATION:
 ; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 ; APPLICANT: Bristol-Myers Squibb, Co.
 ; APPLICANT: Beyer, Stefan
 ; APPLICANT: Bloecker, Helmut
 ; APPLICANT: Brandt, Petra
 ; APPLICANT: Cino, Paul M
 ; APPLICANT: Dougherty, Brian A
 ; APPLICANT: Goldberg, Steven L
 ; APPLICANT: Hoffe, Gerhard
 ; APPLICANT: Mueller, Joachim
 ; APPLICANT: Reichenbach, Hans
 ; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 ; TITLE OF INVENTION: heteropolyketide compounds
 ; FILE REFERENCE: PCT/US 99/23535
 ; CURRENT APPLICATION NUMBER: US/09/413,814
 ; CURRENT FILING DATE: 1999-10-07
 ; PRIOR APPLICATION NUMBER: DE 198 46 493.2
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: Patent in Ver. 2.1

; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30831

Query Match 9.7%; Score 69; DB 4; Length 232;
 Best Local Similarity 25.6%; Pred. No. 7.7;
 Matches .22; Conservative 14; Mismatches 34; Indels 16; Gaps 4;

QY 49 GHRVLPGTGASAIATVTPKASMKLKPQSTKSPEL-----RELRSKIREMNKTIS 102
 DB 121 GHRVLP--AGSRAATARP-----ARPRGSRVAFGIPARSFARVHRRLATLHRQPO 172
 QY 103 QESARVNHRLPEGHPLLEKRAEYFRH 128
 DB 173 PQLRTANGKIP--RPKQTNRSNFHLH 196

RESULT 34
 US-09-252-991A-25526
 ; Sequence 25526 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25526
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25526

Query Match 9.7%; Score 69; DB 4; Length 411;
 Best Local Similarity 30.5%; Pred. No. 17;
 Matches 32; Conservative 12; Mismatches 53; Indels 8; Gaps 5;

QY 14 NRPTFGETDVNRVREALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAI--AATVTPKAS 71
 DB 128 HRPLQESGRLEQLRLR-RAPAHLQRRAGNAGR--TTGGGAAGADRRLRHRQFAP 184
 QY 72 MKLKPQSTKSPELRELSKIREMNKTISQESARVNHRLPEGH 116
 DB 185 RSGRRPRGSPHAGRLRRRRHRRH--RQHPPRPAHRQP-GH 226

RESULT 35
 US-09-252-991A-24836
 ; Sequence 24836 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24836
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24836

Query Match 9.7%; Score 69; DB 4; Length 454;
 Best Local Similarity 28.1%; Pred. No. 19;
 Matches 27; Conservative 13; Mismatches 48; Indels 8; Gaps 3;

QY 26 REALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAIATVTPKASMKLKPQSTK 82
 DB 110 RHQLWRLPGDPQPVARGALAGLAGADLPRRGLADAAARPRGSORIPQDPQGRQP 169
 QY 83 KSPERELSRKIREMNKTISQESARVNH-----RLP 113
 DB 170 SPAGLRGIPRCAAGGVVROLCAALDHHFFRRRLP 205

RESULT 36
 US-09-252-991A-32102
 ; Sequence 32102 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 32102
 ; LENGTH: 461
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-32102

Query Match 9.7%; Score 69; DB 4; Length 451;
 Best Local Similarity 26.8%; Pred. No. 20;
 Matches 30; Conservative 15; Mismatches 57; Indels 10; Gaps 3;

QY 25 MREALLRVKSSERLAMLRLALA-GMCGHRVLPFGTGASAIATVTPKASMKLKPQSTK 83
 DB 309 LRQPAQVAYGQALAEQFVLALGTAGHRAAPAQAQHA-----KGAAGHLHPRHVERQ 361
 QY 84 SPBLRELSKIREMNKTISQESARVNHRLPEGHPLLEKRAEYFRHLRLSKSO 135
 DB 362 GMEVEEPFAD--EIADTIQGVRAEHGDFLGAADOVHLRFRPLQVERPQ 411

RESULT 37
 US-09-413-814-3
 ; Sequence 3 Application US/09413814
 ; Patent No. 6225064
 ; GENERAL INFORMATION:
 ; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 ; APPLICANT: Bristol-Myers Squibb, Co.
 ; APPLICANT: Beyer, Stefan
 ; APPLICANT: Bloecker, Helmut
 ; APPLICANT: Brandt, Petra
 ; APPLICANT: Cino, Paul M
 ; APPLICANT: Dougherty, Brian A
 ; APPLICANT: Goldberg, Steven L
 ; APPLICANT: Hoffe, Gerhard
 ; APPLICANT: Mueller, Joachim
 ; APPLICANT: Reichenbach, Hans
 ; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 ; TITLE OF INVENTION: heteropolyketide compounds
 ; FILE REFERENCE: PCT/US 99/23535
 ; CURRENT APPLICATION NUMBER: US/09/413,814
 ; CURRENT FILING DATE: 1999-10-07
 ; EARLIER APPLICATION NUMBER: DE 198 46 493.2
 ; EARLIER FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-3

Query Match 9.7%; Score 69; DB 3; Length 553;
Best Local Similarity 24.3%; Pred. No. 26;
Matches 34; Conservative 15; Mismatches 61; Indels 30; Gaps 4;

QY 11 VAENRPTFGTFDYMREALLVKSSERLAMLRLALAGMCGHRVLPGTGASAIATVTPKA 70
Db 259 VLEPPRLGELRDGIPRPL-----ERL-VARMLAKNAGERPRDGAALAAVAGEGL 311

QY 71 SMKLPKPPRPOSTKSPRLSRLSKL-----RENNKTIISQESARVNRHLPFGHPLLE 120
Db 312 SIGASVAAPAAPEAITTAERKVMCVILAEADGGAAGATLSEDDGAA----- 359

QY 121 KRAEYFRHLRLSKSQGVNRL 140
Db 360 -RAEALRDIAARHGRLDRL 378

RESULT 38
US-07-977-434-8
; Sequence 8, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: Wordperfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977.434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 834 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-977-434-8

Query Match 9.7%; Score 69; DB 1; Length 834;
Best Local Similarity 23.7%; Pred. No. 45;
Matches 44; Conservative 27; Mismatches 53; Indels 62; Gaps 10;

QY 1 MESTSTTTNFVAENRPTFGS-TFDVMREALL-----RVKSSERLAML-----RAL 44
Db 382 LDPSNTTPEGVA--RRYGGWETEDAAHRALLAERLQONLLERLKGEEKLLWLYOEVEKPL 439

QY 45 AGMCGHRVLPGTGASAIATVTPKGMKLPKPPRPOSTKSPRLSRLSKL----- 94
Db 440 SRVLAH--MEATGVRLDVAYL--KALSLEL-----AEBIRLEEVFRLAGHPFNL 486

QY 95 ---RENNKTIISQ-----SARVNRHLPFGHPLLEKRAEYFRHLRLSKS 134
Db 487 NSRDQLERVLFDLRLPALGKTKGRTSAAVLEALREAHPIVEKILQH-RELTKLKN 545

QY 135 QGVNRL 140
Db 546 TVVDPL 551

RESULT 39
US-08-458-819-8
; Sequence 8, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: Wordperfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,819
; FILING DATE: 02-JUN-1995

Query Match	9.7%	Score 69;	DB 1;	Length 834;
Best Local Similarity	23.7%;	Pred. NO. 45;		
Matches	44;	Conservative 27;	Mismatches 53;	Indels 62; Gaps 10;
QY	1	MESTSTTNFVAENRPTFGE--TFDVREALL-----RVKSGSERLAMI-----RAL	44	
Db	382	LDPSNTTPEGVA--RRYCGGWTEDAAHRALLAERLQNLLERLKGEKLLMLYQVEKPL	439	
QY	45	AGMCHRVLPOTGASAJAATAVTPKGASMKLKP RPPOSTKSPELRELSRKI-----	94	
Db	440	SRVLAH--MEATGVRLDVAVL--KALSLEL-----AEBIRLEEVEVFRLAGHPENL	486	
QY	95	---REMNKTIQS-----SARVNHRLPEGHPLKEKAAEVFRHLRSUKS	134	
Db	487	NSRDOLSERVDFELRLPALGKTOKTKGRSTAAVLEALREAHPIVEKILQH--REITKLEN	545	
QY	135	QGVNRL	140	

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 834 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-07035-8

Query Match          9.7%; Score 69; DB 5; Length 834;
Best Local Similarity 23.7%; Pred. NO. 45;
Matches 44; Conservative 27; Mismatches 53; Indels 62; Gaps 10;

QY 1 MESTSTTNFVAENRPTFGE-TFDVMREALL-----RVKSSERLAML-----RAL 44
Db 382 LDPSNTTPEGVA--RRYGEWTEDAAHALLAERLQONLLERLKGEEKLLWLYQVEVKPL 439
QY 45 AGMCGHRLVPTGTGASAIATVTPKGASMKLXPPRPQSTKSPELRELSRKI----- 94
Db 440 SRVLAH--MEATGVRLDVAYL--KALSLEL-----AEEIRLEEVEVFRLAGHPFNL 486
QY 95 ---REMNKTISOE-----SARVNHRLPEGHPLLEKRAEYFRHLRSIKS 134
Db 487 NSRDQLERVLFDLELRLPALGKTQTKGRKSTSAANVLEALREAHPIVEKILQH-RELTCLKN 545
QY 135 QGVNRL 140
Db 546 TYVDPL 551
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Search completed: November 14, 2003, 10:43:08
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:41:46 ; Search time 30 Seconds
(without alignments)

858.030 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 708
Sequence: 1 MESTSTTNFVAENRPTGEE.....RAEYFRLRLSLKSGQVNRLLI 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	141	12	US-10-087-573-2
2	638	90.1	285	12	Sequence 2, Appli
3	77	10.9	192	12	Sequence 4, Appli
4	75.5	10.7	839	11	Sequence 180, App
5	75.5	10.7	839	12	Sequence 47, Appl
6	75.5	10.7	839	12	Sequence 202, App
7	73.5	10.4	293	10	Sequence 47, Appl
8	73.5	10.4	293	10	Sequence 231, App
9	73.5	10.4	293	10	Sequence 231, App
10	73.5	10.4	293	10	Sequence 231, App
11	73.5	10.4	293	11	Sequence 231, App
12	73.5	10.4	293	11	Sequence 231, App
13	73.5	10.4	293	11	Sequence 231, App
14	73.5	10.4	293	11	Sequence 231, App
15	73.5	10.4	293	11	Sequence 231, App

16	73.5	10.4	293	11	US-09-978-564A-231	Sequence 231, App
17	73.5	10.4	293	11	US-09-999-833A-231	Sequence 231, App
18	73.5	10.4	293	11	US-09-981-915A-231	Sequence 231, App
19	73.5	10.4	293	11	US-09-978-824-231	Sequence 231, App
20	73.5	10.4	293	11	US-09-918-585A-231	Sequence 231, App
21	73.5	10.4	293	11	US-09-978-423A-231	Sequence 231, App
22	73.5	10.4	293	11	US-09-978-193A-231	Sequence 231, App
23	73.5	10.4	293	11	US-09-999-830A-231	Sequence 231, App
24	73.5	10.4	293	11	US-09-978-757A-231	Sequence 231, App
25	73.5	10.4	293	11	US-09-978-187B-231	Sequence 231, App
26	73.5	10.4	293	11	US-09-978-643A-231	Sequence 231, App
27	73.5	10.4	293	12	US-09-978-375A-231	Sequence 231, App
28	73.5	10.4	293	12	US-09-978-188A-231	Sequence 231, App
29	73.5	10.4	293	12	US-09-978-398A-231	Sequence 231, App
30	73.5	10.4	293	12	US-10-137-870-422	Sequence 422, App
31	73.5	10.4	293	12	US-10-140-018-422	Sequence 422, App
32	73.5	10.4	293	12	US-10-140-021-422	Sequence 422, App
33	73.5	10.4	293	12	US-10-140-274-422	Sequence 422, App
34	73.5	10.4	293	12	US-10-140-471-422	Sequence 422, App
35	73.5	10.4	293	12	US-10-140-807-422	Sequence 422, App
36	73.5	10.4	293	12	US-10-140-922-422	Sequence 422, App
37	73.5	10.4	293	12	US-10-140-924-422	Sequence 422, App
38	73.5	10.4	293	12	US-10-140-926-422	Sequence 422, App
39	73.5	10.4	293	12	US-10-141-698-422	Sequence 422, App
40	73.5	10.4	293	12	US-10-141-702-422	Sequence 422, App
41	73.5	10.4	293	12	US-10-141-704-422	Sequence 422, App
42	73.5	10.4	293	12	US-10-142-421-422	Sequence 422, App
43	73.5	10.4	293	12	US-10-142-432-422	Sequence 422, App
44	73.5	10.4	293	12	US-10-142-767-422	Sequence 422, App
45	73.5	10.4	293	12	US-10-143-031A-231	Sequence 231, App

ALIGNMENTS

RESULT 1
US-10-087-573-2
; Sequence 2, Application US/10087573
; Publication No. US20030165872A1
; GENERAL INFORMATION:
; APPLICANT: SCHEITERS, Theodorius PM
; APPLICANT: CARCY, Bernard PD
; APPLICANT: DRACULOVSKI, Pascal R
; APPLICANT: GORENFLOT, Andre F
; TITLE OF INVENTION: BABESIA CANIS VACINE
; FILE REFERENCE: SCHEITERS
; CURRENT APPLICATION NUMBER: US/10/087,573
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: EP 01200816.5
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Babesia canis
US-10-087-573-2

Query Match	100.0%	Score 708;	DB 12;	Length 141;
Best Local Similarity	100.0%	Pred. No. 1e-65;		
Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MESTSTTNFVAENRPTGEEFDVNRALLRVKSSERLAMLALAGMCHRVLPOTGASA	60	
DB	1	MESTSTTNFVAENRPTGEEFDVNRALLRVKSSERLAMLALAGMCHRVLPOTGASA	60	
QY	61	IAATVTPKASMKLPPRQSTKSPDLRLKIREMKNKTSQESARVNHRLPEGHPLLE	120	
DB	61	IAATVTPKASMKLPPRQSTKSPDLRLKIREMKNKTSQESARVNHRLPEGHPLLE	120	
QY	121	KRAEYFRLRLSLKSGQVNRLLI	141	
DB	121	KRAEYFRLRLSLKSGQVNRLLI	141	

RESULT 2
US-10-087-573-4
; Sequence 4, Application US/10087573
; Publication No. US20030165872A1
; GENERAL INFORMATION:
; APPLICANT: SCHEITERS, Theodorius PM
; APPLICANT: CARCY, Bernard PD
; APPLICANT: DRACULOVSKI, Pascal R
; APPLICANT: GORENLOT, Andre F
; TITLE OF INVENTION: BABESIA CANIS VACCINE
; FILE REFERENCE: SCHEITERS
; CURRENT APPLICATION NUMBER: US/10/087.573
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: EP 01200816.5
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Babesia canis
US-10-087-573-4

Query Match 90.1%; Score 638; DB 12; Length 285;
Best Local Similarity 94.8%; Pred. No. 4.8e-56;
Matches 128; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MESTSTTNFVAENRPTFGTDFVREALLRVKSSERLALAGMCHGRVLPFGTGASA 60
DB 1 MESTSTTNFVAENRPTFGTDFVREALLRVKSSERLALAGMCHGRVLPFGTGASA 60

QY 61 IAAVTGKASMKLPKPPPOSTKSPPELRSKIRENMKTIISOESARVNHRLPEGHPLLE 120
DB 61 IAAVTGKASMKLPKPPPOSTKSPPELRSKIRENMKTIISOESARVNHRLPEGHPLLE 120

QY 121 KRAEYFRHLRSLSQ 135
DB 121 KRAEYFVTLDLRAK 135

RESULT 3
US-10-190-435-180
; Sequence 180, Application US/10:90435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190.435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vif HXB2
US-10-190-435-180

Query Match 10.9%; Score 77; DB 12; Length 192;
Best Local Similarity 27.9%; Pred. No. 4.9;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMVREALLRVKSSERLALAGMCHGRVLPFGTGASAIATVTPKGASW 72
DB 22 FDMVREALLRVKSSERLALAGMCHGRVLPFGTGASAIATVTPKGASW 72

DB 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK----- 157

QY 73 KLPKPPPOSTKSPPELRSKIRENMKTIISOESARVNHRLPEGH 116
DB 156 KIKPPLPSVTKLTEDR-----WNKPKTKGHRGSHM-NGH 192

RESULT 4
US-09-864-636A-47
; Sequence 47, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwail, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864.636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-47

Query Match 10.7%; Score 75.5; DB 11; Length 839;
Best Local Similarity 28.3%; Pred. No. 51;
Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 8;

QY 29 LLRVKSSERLAML-----RALAGMCHGRVLPOTGA-----SAIAATVTPKGASMKLP 76
DB 418 LKRLEGEERLLWLYREVERPLSAVLAH--MEATGVRLDVAVLRALSLEVAEEIARLEAEV 475

QY 77 PR-----POSTKSPPELRSR-----KIRENMKTIISOE-SARVNHRLPEGHPLLEKR 122
DB 476 FRLAGHPNLSRD--QLERVLFDELRIPIKIKKTKRSTSAVLEALREAHFIVEKI 533

QY 123 AEYFRHLRSLSQGVNRL 140
DB 534 LQY-RELTKLKSTYIDPL 550

RESULT 5
US-09-758-282-202
; Sequence 202, Application US/09758282
; Publication No. US20030134349A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Wu-Po
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamicheva, Natalie E.
; APPLICANT: Allwail, Hatim T.
; APPLICANT: Schaefer, James J.
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Improved Enzymes for the Detection of Specific Nucleic
; FILE REFERENCE: FORS-04323
; CURRENT APPLICATION NUMBER: US/09/758.282
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-282-202

Query Match 10.7%; Score 75.5; DB 12; Length 839;
 Best Local Similarity 28.3%; Pred. No. 51;
 Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 8;

QY 29 LRVKSSERLAML-----PALAGMCHRVLPOTGA-----SAIAATVTPKGASMKLKP 76
 DB 418 LKRLGGEERLLWLYREVERPLSAVLAH--MEATGVRLDVAVLRALSLEVAEIALEAEV 475
 QY 77 PR-----POSTKSPPELRELSR-----KIREMKNKTISQE--SARVNHRLPEGHPLEK 122
 DB 476 FRLAGHPFNLSRD--QLERVLFDLRLPKIKKTHKTKRSTSAAVLEALREAHPIVEKI 533
 QY 123 AEFYFRLHRLSLKSGQVNR 140
 DB 534 LQY-RELTKLKSTYIDPL 550

RESULT 6

US-10-084-839-47
 ; Sequence 47, Application US/10084839
 ; Publication No. US20030186238A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Third Wave Technologies
 ; APPLICANT: Allawi, Hatim
 ; APPLICANT: Argue, Brad T.
 ; APPLICANT: Bartholomay, Christian T.
 ; APPLICANT: Chehak, LuAnne
 ; APPLICANT: Curtis, Michelle L.
 ; APPLICANT: Eis, Peggy S.
 ; APPLICANT: Hall, Jeff G.
 ; APPLICANT: Ip, Hon S.
 ; APPLICANT: Ji, Lin
 ; APPLICANT: Kaiser, Michael
 ; APPLICANT: Kwiatkowski, Jr., Robert W.
 ; APPLICANT: Lukowiak, Andrew A.
 ; APPLICANT: Lyamichev, Victor
 ; APPLICANT: Lyamicheva, Natalie E.
 ; APPLICANT: Ma, WuPo
 ; APPLICANT: Neri, Bruce P.
 ; APPLICANT: Olson, Sarah M.
 ; APPLICANT: Olson-Munoz, Marilyn C.
 ; APPLICANT: Schaefer, James J.
 ; APPLICANT: Skrzypczynski, Zbigniew
 ; APPLICANT: Takova, Tsetska Y.
 ; APPLICANT: Thompson, Lisa C.
 ; APPLICANT: Vedvik, Kevin L.
 ; TITLE OF INVENTION: RNA Detection Assays
 ; FILE REFERENCE: FORS-06666
 ; CURRENT APPLICATION NUMBER: US/10/084,839
 ; CURRENT FILING DATE: 2002-02-26
 ; NUMBER OF SEQ ID NOS: 4004
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 47
 ; LENGTH: 839
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-084-839-47

Query Match 10.7%; Score 75.5; DB 12; Length 839;
 Best Local Similarity 28.3%; Pred. No. 51;
 Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 8;

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 DB 418 LKRLGGEERLLWLYREVERPLSAVLAH--MEATGVRLDVAVLRALSLEVAEIALEAEV 475
 QY 77 PR-----POSTKSPPELRELSR-----KIREMKNKTISQE--SARVNHRLPEGHPLEK 122
 DB 476 FRLAGHPFNLSRD--QLERVLFDLRLPKIKKTHKTKRSTSAAVLEALREAHPIVEKI 533

QY 123 AEFYFRLHRLSLKSGQVNR 140
 DB 534 LQY-RELTKLKSTYIDPL 550
 RESULT 7
 US-09-978-295A-231
 ; Sequence 231, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
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 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078939
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294

RESULT 8

US-09-978-697-231

Sequence 231, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

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APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2630P1C27

CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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PRIOR APPLICATION NUMBER: 60/078939

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Gao, Wei-Qiang
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

PRIOR APPLICATION NUMBER: 60/079664
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US-09-978-192A-231
; Sequence 231, Application US/09978192A
; Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmitted
; TITLE OF INVENTION: Acids Encoding tRNA
; FILE REFERENCE: P2630PLC9
CURRENT APPLICATION NUMBER: US/09/978192A
CURRENT FILING DATE: 2001-10-15
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RESULT 9

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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 10; Length 293;
 Best Local Similarity 28.8%; Pred. No. 20;
 Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

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Db	69	LLRTNASKQTALGALKKEVGDC-HSCCSGTOAQL-----	QTTA--	107
Qy	86	ELRELSRKIREMKNKTISQESAVNNHLP	GHPLLEKRAEYFHLRLSKSQ	135
Db	108	ELGEAQAKLMEQESALRELRERVTOGLAAGRGREDVTFELFALEAVRIQ	158	

RESULT 10
 US-09-999-832A-231
 ; Sequence 231, Application US/09999832A
 ; Publication No. US20020192706A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545

; PRIOR FILING DATE: 1998-04-29
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 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083558
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
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 ; PRIOR APPLICATION NUMBER: 60/085579
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 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 10; Length 293;
 Best Local Similarity 28.8%; Pred. No. 20;
 Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;
 QY 29 LLRVKSERLAMLRL---AGMCHRVLPQTGASALAAATVTPKGASMKLPPRPOSTKSP 85
 DB 69 LLRTNASKTALGALKKEVGDG-HSCSCGTQQL-----QTTRA- 107
 QY 86 ELRELGRKTRENNKTTQSASRVNHLRPE-GHPLLEKRAEYFRLHLSKSQ 135
 DB 108 ELGEAQAKLMEQESALRELRRVTOGLAEAGRGREDVTRFELFRAEAVRLQ 158

RESULT 11

US-09-978-189-231
 ; Sequence 231, Application US/09978189
 ; Publication No. US2003004102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C7
 ; CURRENT APPLICATION NUMBER: US/09/978,189
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
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 ; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/083742
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAWLRAL---AGMCGHRVLPGTGASAIATVTPKGASMKLKPFPQSTKSP 85
DB 69 LLRTNASKQTAAALGALKEEVGDC-HSCCSGTQAOQ-----QTTRA- 107
QY 86 ELRELSRKIREMNKNTISQESARVNHRLPE-CHPLLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELREVRTQGLAEAGRGREDVTELFRALEAVRLQ 158

RESULT 12
US-09-978-608A-231
; Sequence 231, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan

```

; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,508A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 231
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-508A-231

Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPOTGASAIATVTPKGASMKLKPPRQSTKSP 85
Db 69 LLRTNASKQTALGALKKEVGDC-HSCCSTQACL-----OTTRA- 107

QY 86 ELRLSRKIREMNKTTISQESARVNNHRLPE-GHPLLEKRAEYFRHLRLSLKSO 135
Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAEAGRGREDVTELFRALAEVRLQ 158

RESULT 13
US-09-978-585A-231
; Sequence 231, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 231
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-231

Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPOTGASAIATVTPKGASMKLKPPRQSTKSP 85
Db 69 LLRTNASKQTALGALKKEVGDC-HSCCSTQACL-----OTTRA- 107

QY 86 ELRLSRKIREMNKTTISQESARVNNHRLPE-GHPLLEKRAEYFRHLRLSLKSO 135
Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAEAGRGREDVTELFRALAEVRLQ 158

RESULT 14
US-09-978-191A-231
; Sequence 231, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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PRIOR APPLICATION NUMBER: 60/081955	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13

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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LRVKSSERLAMLRL---AGNCGRHVLPGTGASAIATAATVTPKGSMKLGKPRPQSTKSP 85
DB 69 LLRTNASKQTAALGALKVEVGC-HSCCSGTQACL-----QTTRA- 107
QY 86 ELRELSKIREMNKTIISOESARVNHRLPE-GHPLLEKEAEVFRHLRLSKSQ 135
DB 108 ELGEAAQLMEQESALRELRLRVRTQTGLAEAGRGREDVRLTFRALEAVRLQ 158

RESULT 15
US-09-978-403A-231
; Sequence 231, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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1  APPLICANT: WOOD, WILLIAM L.
2  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
3  ACIDS ENCODING THE SAME
4  TITLE OF INVENTION: Acids Encoding the Same
5  FILE REFERENCE: P2630P1C25
6  CURRENT APPLICATION NUMBER: US/09/978,564A
7  CURRENT FILING DATE: 2001-10-16
8  PRIOR APPLICATION NUMBER: 09/918585
9  PRIOR FILING DATE: 2001-07-30
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13 PRIOR FILING DATE: 1997-11-03
14 PRIOR APPLICATION NUMBER: 60/065311
15 PRIOR FILING DATE: 1997-11-13
16 PRIOR APPLICATION NUMBER: 60/066364

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73	PRIOR APPLICATION NUMBER: 60/085689	

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatch 41; Indels 25; Gaps 5;

QY 29 LRVKSSERLMLRAL---AGMCHRVLPCTGSAIAAATVTKGASMKLKPPRPSTKSP 85
DB 69 LLRTNASKQTALGALKVEGDC-HSCSGTQACL-----QTTRA- 107
QY 86 ELRELSRKREMNKTIQSARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAAKLMEQESALRELRERTVQGLAEAGRGREDVRTLFRALAEAVELQ 158

RESULT 17
US-09-999-833A-231
; Sequence 231, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1065
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred.No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;
Qy 29 LLRVKSERLAMLRL---AGMCHRVLPOTGASAIATVTGKSMKLPKPPQSTKSP 85
Db 69 LLRTNASKQTAAALCALKEEVGDC-HSCCSGTQAL-----QTTA- 107
Qy 86 ELRELSRKIREMNKTIQSASRVNHLRPE-GHPLLEKRAEYFRLRLSLKXQ 135
Db 108 ELGEAQAKLMEQESALRELRLRVVTQGLAEAGRGREDVRLTFLRALEAVRLQ 158

RESULT 18

US-09-981-915A-231
; Sequence 231, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 05/918585
; PRIOR FILING DATE: 2001-07-20
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
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Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSERLMLRAL--AGMCHRVLPCTGASAIATVTPKGASMKLPPRPOSTKSP 85
DB 69 LRTNASKOTAAALGALKEEVGDC-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIRENMKTTISQBSARNVHRLPE-GHPLLEKRAEYFRHLRSLKSQ 135
DB 108 ELCEAOAKLMEQESALRELRRVTOGLABAGRGREDVRTLFRALFAVRLQ 158

RESULT 19
US-09-978-824-231
; Sequence 231, Application US/09978824
; Publication No. US2003005216A1
; GENERAL INFORMATION:
; APPLICANT: Aehkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/082704
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; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRLVPGTGASAIATVTPKGASMKLPPRPQSTKSP 85
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|: |||
DB 69 LLRTNASKQTAALGALKKEVGDC-HSCCSGTQAQL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
   ||| ||| :|: ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 108 ELGEAQAKLMEQESALRELRERVTOGLAEAGRGREDVYRTFLFAELAVRLQ 158

RESULT 20
US-09-918-585A-231
; Sequence 231, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C1
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886

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;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082796
;; PRIOR FILING DATE: 1998-04-23
;; PRIOR APPLICATION NUMBER: 60/083336
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR APPLICATION NUMBER: 60/083495
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;; PRIOR APPLICATION NUMBER: 60/083545
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;; PRIOR APPLICATION NUMBER: 60/083554
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLMLRAL---AGMCGHRVLPQTGASALAAATVTPKGASMKLPPRPQSTKSP 85
Db 69 LLRTNASKQTAALGALKKEVGDC-HSCCSGTQAL-----QITRA- 107
Qy 86 ELRELGRKIREMNKTIQSASRVNHLPE-GHPLLEKRAEYFHLRLSLKSQ 135
Db 108 ELGEAQAKLMEQESALRELREVRTQGLAEAGRGREDVRLTELFALEAVRLQ 158

RESULT 22

US-09-978-193A-231
; Sequence 231, Application US/09978193A
; Publication No. US20030073624A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PLC6
; CURRENT APPLICATION NUMBER: US/09/978,193A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910

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60/0857005	PRIOR FILING DATE: 1998-05-15
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60/0856978	PRIOR FILING DATE: 1998-05-15

Qy 29 LLRVKSSERLAMLRAL---AGMCGHVLPGTCASAIATVTPGASMCLKPPRPOSTKSP 85
||| : :: ||| | | | | |
Db 69 LLRTNASQTALGALKKEVGDC-HSCCSGTQAQL-----QTTRA-10
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QY 86 ELRELSRKIREMNKTIQESARVNHRLPE-GHPLEKRAEYRHLRLSKSQ 135
Db 108 ELGEAQKLMQESALREURRVTQGLAAGRGREDVIRTELFRALFAVLQ 158

RESULT 23

US-09-999-830A-231
; Sequence 231, Application US/09999830A
; Publication No. US2003007700A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC70
; CURRENT APPLICATION NUMBER: US/09/999,830A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR FILING DATE: 1998-03-13
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; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322

108 ELCEAQAQKLMEQESALRELPRVTTQGLAEAGRGREDVRTLELFALEAVRLQ 158
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 RESULT 24
 US-09-978-757A-231
 ; Sequence 231, Application US/09978757A
 ; Publication No. US20030083248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secrets and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC26
 ; CURRENT APPLICATION NUMBER: US/09/978,757A
 ; CURRENT FILING DATE: 2002-03-19
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;

Best Local Similarity 28.8%; Pred. No. 20;

Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLAMLRAL---AGMCGHRYLPCTGASATAATVTPKGASMKLPPRPQSTKSP 85

Db 69 LLRTNASKQTAAALCALKEEVGDC-HSCCSTQAL-----QTFRA-107

Qy 86 ELRELSKIREMKNKTSQESARVNNHRLPE-CHPLEKRAEYFHLRLSKSQ 135

Db 108 ELGEAQAKLMEQESALRELRERVTOGLAEAGRGREDVRLTFLFALEAVRLQ 158

RESULT 25

US-09-978-187B-231
; Sequence 231, Application US/09978187B
; Publication No. US2003009674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Pacini, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C5
; CURRENT APPLICATION NUMBER: US/09/978.187B
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; Publication No. US20030104998A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kujavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C16
; CURRENT APPLICATION NUMBER: US/09/978,643A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 231
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-643A-231

Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLMLRAL---AGMCGHRVLPCTGASALAAATVTPKGASMKLPPRPOSTKSP 85
DB 69 LLRTNASKQTALGALKEEVGDC-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIREMNKTIQSASRVNHLRPE-GHPLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELRERVTOGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 27
US-09-978-375A-231
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; Publication No. US20030130181A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

; Publication No. US20030104998A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 12; Length 293;

Best Local Similarity 28.8%; Pred.No.20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLAMLRL--AGMCGHVRVLPQTGASAJAATVTPKGSMKLPKPPRQSTKSP 85

Db 69 LLRTNASKQTAALGALKKEVGDG-HSCCSTQAL-----QITRA- 107

Qy 86 ELRELSKIRENMKNTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135

Db 108 ELGEAQAKLMEQESALRELREVRTQGLAEAGRGREDVRLTFLRALEAVRLQ 158

RESULT 29

US-09-978-298A-231
; Sequence 231, Application US/09978298A

; Publication No. US20030134785A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C2

; CURRENT APPLICATION NUMBER: US/09/978,298A

us-10-087-573-2.rapb

PRIOR APPLICATION NUMBER: 60/081200	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-07

; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085582
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085700
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085689
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 12; Length 293;
 Best Local Similarity 28.8%; Pred. No. 20;
 Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLMLRAL---AGMCGHRVLPGTGASAIATVTPKGSMKLPKPPRQSTKSP 85
 Db 69 LLRTNASKQTAAALGALKEEVGDC-HSCCSGTQACL-----QTTRA- 107
 Qy 86 ELRELSRKIRENMKNTISQESARVNHRLPE-GHPLEKRAEYFRHLRLSKSQ 135
 Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAAGRGREDVRLTFRALEAVRLQ 158

RESULT 30

US-10-137-870-422
 ; Sequence 422, Application US/10137870
 ; Publication No. US2003013883A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C155

; CURRENT APPLICATION NUMBER: US/10/137,870

; CURRENT FILING DATE: 2002-05-03

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 422

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-137-870-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
 Best Local Similarity 28.8%; Pred. No. 20;
 Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLMLRAL---AGMCGHRVLPGTGASAIATVTPKGSMKLPKPPRQSTKSP 85
 Db 69 LLRTNASKQTAAALGALKEEVGDC-HSCCSGTQACL-----QTTRA- 107
 Qy 86 ELRELSRKIRENMKNTISQESARVNHRLPE-GHPLEKRAEYFRHLRLSKSQ 135
 Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAAGRGREDVRLTFRALEAVRLQ 158

RESULT 31

US-10-140-018-422
 ; Sequence 422, Application US/10140018
 ; Publication No. US20030138885A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C158

; CURRENT APPLICATION NUMBER: US/10/140,018

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 422

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-018-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
 Best Local Similarity 28.8%; Pred. No. 20;
 Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLMLRAL---AGMCGHRVLPGTGASAIATVTPKGSMKLPKPPRQSTKSP 85
 Db 69 LLRTNASKQTAAALGALKEEVGDC-HSCCSGTQACL-----QTTRA- 107
 Qy 86 ELRELSRKIRENMKNTISQESARVNHRLPE-GHPLEKRAEYFRHLRLSKSQ 135
 Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAAGRGREDVRLTFRALEAVRLQ 158

RESULT 32

US-10-140-021-422
 ; Sequence 422, Application US/10140021
 ; Publication No. US20030138886A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven

```

; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCHRVLPGTGASAIATVTPKGSMKLPKPPQSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTIQESARVNNHRLPE-GHPLEKRAEYFRHLRSLSKQ 135
DB 108 ELGEAQAKLMEQESALRELRLERVTOGLAEAGRGREDVRTLFRALFAVRLQ 158

RESULT 34
US-10-140-471-422
; Sequence 422, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCHRVLPGTGASAIATVTPKGSMKLPKPPQSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTIQESARVNNHRLPE-GHPLEKRAEYFRHLRSLSKQ 135
DB 108 ELGEAQAKLMEQESALRELRLERVTOGLAEAGRGREDVRTLFRALFAVRLQ 158

RESULT 35
US-10-140-807-422
; Sequence 422, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
```

APPLICANT: Tamas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C174
CURRENT APPLICATION NUMBER: US/10/140,807
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 422
LENGTH: 293
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-807-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPCTGASAIATVTPKGASMKLKP RPQSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDG-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISOESARVNHRLPE-GHPLLEKRAEYFRHLRSLSKQ 135
DB 108 ELGEAQAKLMEQSAALRELRVVTQGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 36
US-10-140-922-422
Sequence 422, Application US/10140922
Publication No. US2003013889A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C177
CURRENT APPLICATION NUMBER: US/10/140,924
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 422
LENGTH: 293
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-924-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPCTGASAIATVTPKGASMKLKP RPQSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDG-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISOESARVNHRLPE-GHPLLEKRAEYFRHLRSLSKQ 135
DB 108 ELGEAQAKLMEQSAALRELRVVTQGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 38
US-10-140-926-422
Sequence 422, Application US/10140926
Publication No. US20030134356A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K

QY 86 ELRELSRKIREMKNKTISOESARVNHRLPE-GHPLLEKRAEYFRHLRSLSKQ 135
DB 108 ELGEAQAKLMEQSAALRELRVVTQGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 37
US-10-140-924-422
Sequence 422, Application US/10140924
Publication No. US2003013435A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C177
CURRENT APPLICATION NUMBER: US/10/140,924
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 422
LENGTH: 293
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-924-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPCTGASAIATVTPKGASMKLKP RPQSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDG-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISOESARVNHRLPE-GHPLLEKRAEYFRHLRSLSKQ 135
DB 108 ELGEAQAKLMEQSAALRELRVVTQGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 38
US-10-140-926-422
Sequence 422, Application US/10140926
Publication No. US20030134356A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K

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; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-926-422

Query Match      10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCHRVLPGTGASAIATVTPKGASMKLKPPRPOSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRLSKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRSLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELRLRVRTQGLAEAGRGREDVRTLFRALFAVRLQ 158

RESULT 39
US-10-141-698-422
; Sequence 422, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C206
; CURRENT APPLICATION NUMBER: US/10/141,698
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-698-422

Query Match      10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCHRVLPGTGASAIATVTPKGASMKLKPPRPOSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRLSKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRSLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELRLRVRTQGLAEAGRGREDVRTLFRALFAVRLQ 158

RESULT 40
US-10-141-702-422
; Sequence 422, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C208
; CURRENT APPLICATION NUMBER: US/10/141,702
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-702-422

Query Match      10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCHRVLPGTGASAIATVTPKGASMKLKPPRPOSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRLSKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRSLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELRLRVRTQGLAEAGRGREDVRTLFRALFAVRLQ 158

Search completed: November 14, 2003, 10:49:28
Job time : 31 secs
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4.

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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:35 ; Search time 43 Seconds
(without alignments)
315.344 Million cell updates/sec

Title: US-10-087-573-2
Perfect score: 708
Sequence: 1 MESSTTTFVAENRPTFGE.....RAEYFRLRLSLKSGVNRLLI 141
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	12.1	524	A75588	probable protein k
2	84.5	11.9	609	A43906	nuclear phosphopro
3	82	11.6	192	S33981	vif protein - huma
4	82	11.6	239	AG2057	hypothetical prote
5	81.5	11.5	1281	G83405	hypothetical prote
6	81	11.4	192	S42996	viral infectivity
7	80	11.3	464	C83328	hypothetical prote
8	80	11.3	902	T98878	respiratory burst
9	79.5	11.2	3839	T49799	related to TOM1 pr
10	79	11.2	192	S42944	viral infectivity
11	79	11.2	192	S42957	viral infectivity
12	79	11.2	1780	T17272	hypothetical prote
13	78.5	11.1	92	S61809	Malike protein enn
14	78.5	11.1	1120	F90693	mechanosensitive c
15	78.5	11.1	1120	B85544	probable membrane
16	78.5	11.1	1120	H84776	hypothetical prote
17	78	11.0	171	D96547	viral infectivity
18	78	11.0	192	S42959	viral infectivity
19	78	11.0	686	F72655	hypothetical prote
20	77.5	10.9	480	A45339	outer capsid prote
21	77	10.9	192	ASLJ83	vif protein - huma
22	77	10.9	192	ASLJNA	vif protein - huma
23	77	10.9	192	S42960	viral infectivity
24	77	10.9	192	S42960	viral infectivity
25	77	10.9	192	S42940	viral infectivity
26	77	10.9	192	S42946	viral infectivity
27	77	10.9	889	H84506	probable retroelem
28	76	10.7	192	S42977	viral infectivity
29	76	10.7	325	E85966	probable aldehyde

30 76 10.7 405 2 E82992
31 76 10.7 408 2 G70522
32 76 10.7 427 2 I49603
33 76 10.7 1021 2 G75403
34 75.5 10.7 350 2 F97169
35 75 10.6 192 2 S43000
36 75 10.6 192 2 S42965
37 75 10.6 606 2 G75302
38 75 10.6 1313 2 A48467
39 75 10.6 1957 2 A45627
40 74.5 10.5 288 2 AE2083
41 74.5 10.5 938 2 T39006
42 74.5 10.5 1006 2 T42731
43 74 10.5 682 2 D54078
44 74 10.5 908 1 JQ1938
45 73.5 10.4 402 2 S37046

ALIGNMENTS

RESULT 1

A75588
probable protein kinase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: A75588
R:White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75588
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-524 <WHI>
A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12449.1; PID:g6460
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0332
A:Map position: 2

Query Match 12.1%; Score 86; DB 2; Length 524;
Best Local Similarity 29.0%; Pred. No. 4.5;
Matches 29; Conservative 23; Mismatches 28; Indels 20; Gaps 6;
QY 25 MREALL-----RVKSSERLAMLALAGMCHRYLPGTG-----ASAIAATVTPKGSMKLK 75
DB 287 LREAVLSCHMAPRIENRPSA--QAL-----RRILRGEGVTVTAPAAPAPQSQPVR 339
QY 76 P---PRPQSTKSPEL-RELSRKIREMNKTIQSBSARVNHR 111
DB 340 PSPAPTPTMPENQTDREVEKRLUREKEVRKEARRQSR 379

RESULT 2

A43906
nuclear phosphoprotein xnf7 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C:Accession: A43906; S27947
R:Reddy, B.A.; Kloc, M.; Eskin, L.
Dev. Biol. 148, 107-116, 1991
A:Title: The cloning and characterization of a maternally expressed novel zinc finger n
A:Reference number: A43906; MUID:92038424; PMID:1936552
A:Accession: A43906
A:Molecule type: mRNA
A:Residues: 1-609 <RED>
A:Cross-references: EMBL:M63705; NID:g214914; PID:g214915
A>Note: sequence extracted from NCBI backbone (NCBI:64515, NCBI:64520)
C:Genetics:
A:Gene: xnf7

C:Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:141-190/Domain: RING finger homology <RING>

Query Match	11.9%	Score 84.5;	DB 2;	Length 609;
Best Local Similarity	30.9%	Pred. No. 7.4;		
Matches 30;	Conservative 12;	Mismatches 38;	Indels 17;	Gaps 4;

Qy	50	HRVLP-----GTGASAIATVTPKCAKMLKPPRPQSTKSPEL--RLSRKIREWNKTIQ	103
		: : : : :	
Db	255	HNPLPILDVAVGYRRELSAIVAPLEASLKV-----TEQLSSQSDKIEHNNKNSQ	305
Qy	104	ESARVNHRLPPEGHPLLEKRAEAYFRHLRSLKSGVNR	140
Db	306	YKHIATSETEKLHKFLRREE--KLLEQLKQGGENLL	340

```

RESULT 3
S33981
vif protein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C/Accession: S33981
R/Carlini, F.
submitted to the EMBL Data Library, November 1991
A/Reference number: S33979
A/Accession: S33981
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-192 <CAR>
A/Cross-references: EMBL:Z11530; NID:G60192; PID:G60195
C/Superfamily: AIDS vif protein

```

Query March	11.6%	Score 82;	DB 2;	Length 192;
Best Local Similarity	26.8%	Pred No. 3.2;		
Matches 30;	Conservative	9;	Mismatches 33;	Indels 32; Gaps 5;
Cy	22	FDVWREALLRVKSSERLAMLALAG-----MCHRVLPFGTGAASIAATVTPKQASM	72	
Db	112	FDCESEAIR-----NAILGNVVRLSCEYQAGHNKIGSLQYLALAAITPK-----	157	
Cy	73	KLKPPRPOSTKSPELRELSRKIRENKNKTIISGARVNHRLPEGH	116	
Db	158	KIKPELPSPVTKLTEDR-----WNKPQKTGKRRNHTM-NGH	192	

RESULT 4

AG2057
hypothetical protein all2013 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG2057
R:Kakano, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001.
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2057
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-239 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA873712.1; PID:gl7131203; GSFDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2013

```
Query Match      11.6%; Score 82; DB 2; Length 239;
Best Local Similarity 26.9%; Pred. No. 4.1;
Matches 21; Conservative 16; Mismatches 39; Indels 2; Gaps 17;

Qy      61 IAAVTVPKGAMKLPKPQQSTKSPELRSRK--IREMNXTISQESARVNHRLPEGHPL 118
```

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Db      141  I A A S L T P N G C F W N A D P I L P E S P T L A I I Y Q A A R E W V S E Q G S N F T E V R A K V G D S S P Q G Y S N      200

Qy      119  L E K R A E Y F R H L R S L K S Q G      136
      : : | | | | |
Db      201  P D Q L A T L D T H L Q M L T K S G      218

RESULT 5
G83405
hypothetical protein PA1923 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83405
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
  adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li
  .; Lory, S.; Olson, M.V.
  Nature 406, 953-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: G83405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1281 <STO>
A:Cross-references: GB:AE004618; GB:AE004091; NID:G9947912; PIDN:AAG05311.1; GSPDB:GN0
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1923

```

Query Match	11.5%;	Score 81.5;	DB 2;	Length 1281;
Best Local Similarity	28.5%;	Pred. No. 33;		
Matches	35;	Conservative 16;	Mismatches 59;	Indels 13; Gaps 5;
QY	25	MREALLRVKSSER-LA---MLRALAGCMCHRVLPGTGASAIATVTPKGASMKLKPRP	79	
Db	743	LRQQLRARELDRLQADTGTLEALLAGLAGRVAPGGGDPINPQVPSGRNLFAF----	798	
QY	80	QSTKSPSLRELSRKIREMNKTTISOESARVNH--RLPEGHPLLEKRAFYFRHLRSKQGV	137	
Db	799	EADKVPTFAAYEGACAEAFGQLL--ESYPAEHQGEAPEKLAFLWSSTMRHLGIVESQAL	856	
QY	138	NRL 140		
Db	857	HAL 859		

RESULT 6
S42996
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42996
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Accession: S42996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30687; NID:G459611; PIDN:CAA83167.1; PID:G459612
C:Superfamily: AIDS vif protein

	Query Match	11.4%	Score 81	DB 2	Length 192
	Best Local Similarity	25.8%	Pred. No. 3.9		
	Matches 31	Conservative 8	Mismatches 33	Indels 32	Gaps 5
QY	22	FDVNRALLRVKSSERLAMILRALAG-----	-----MCGHRVLPGTGASAIATVTPK	QASM	72
		: : : : : : : : : : : :			
DB	112	FDCFSESAR-----	-----KALIGHVTSPECYQAGHNVKGSQYLALALVTPK		157
QY	73	KLKPPRFQSTKSPBELRSLRKIRENNKTTISOESARVNHRLPEGH		116	
DB	158	KTKEPPLPSVTKLTDLR-----	-----WNKPPQTKGHNENETW-NGH	192	

QY 96 EMNKTISOESARVNHRLPEGHPLLEKR 122
DB 142 FITKTDG-----VTGWPEVEKR 158

RESULT 9

T49799

related to TOM1 protein [imported] - Neurospora crassa

A:Alternate names: protein B11B22.10

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49799

R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakaturu

submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49799

A:Molecule type: DNA

A:Residues: 1-3839 <SCH>

A:Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:B11B22.10

A:Experimental source: BAC clone B11B22; strain OR74A

C:Genetics:

A:Gene: NCSP:B11B22.10

A:Map position: 6

A:Introns: 16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1

Query Match 11.2%; Score 79.5; DB 2; Length 3839;

Best Local Similarity 20.9%; Pred. No. 1.9e+02;

Matches 34; Conservative 26; Mismatches 50; Indels 53; Gaps 7;

QY 16 PTFGTDFVMEALLRVKSSR-----LAMLRLALAGMCHRVLPCTGASAIATVTP 67

DB 3344 PTFGOWDKLSACLSAIRQRDNMLNVAITLLPIESLMVCKNTTL--SDASAVNSNSQ 3401

QY 58 KCASKKLPPRPQS-----TKSPLELRLSR 92

DB 3402 K--EMLTSPPEPEDIAGLFTTTEHRIINELVRHNPVKMGTSFLLVKNPKVLEFDN 3459

QY 93 KIREMNKTIISOESARVNHRLPEGHPL-LEKAEYFRH--LRSL 132

DB 3460 KENYENRSVHSKYQTRHSFP---PLQLQVREHVHFDSPSL 3499

RESULT 10

S42944

viral infectivity factor vif - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999

C:Accession: S42944

R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.

submitted to the EMBL Data Library, March 1994

A:Description: In vivo genetic variability of the HIV-1 gene.

A:Reference number: S42940

A:Accession: S42944

A:Molecule type: DNA

A:Residues: 1-192 <WIB>

A:Cross-references: EMBL:Z30605; NID:G459454; PIDN:CAA83082.1; PID:G459455

C:Superfamily: AIDS vif protein

Query Match 11.2%; Score 79; DB 2; Length 192;

Best Local Similarity 29.0%; Pred. No. 6;

Matches 31; Conservative 10; Mismatches 28; Indels 38; Gaps 6;

QY 22 FDVMEALLRVKSSRLAMLRALAGMCHRVLP-----TGA---SAIAATVTPKG 69

DB 112 FCFDSASIR-----NAILGRVSPSCYQAGHNKVGSLQYLALALITPK- 157

QY 70 ASMKLKPPRPOSTKSPLELRLSRKIREMNKTIISOESARVNHRLPEGH 116

DB 158 ---KIKPLPSPVTKLTEDR-----WNKPQTKGRRGSHTL-NGH 192

RESULT 7

C83328

hypothetical protein PA2548 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83328

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: C83328

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-464 <STO>

A:Cross-references: GB:AE004682; GB:AE004091; NID:G9948598; PIDN:AAG05936.1; GSPDB:GN001

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA2548

Query Match 11.3%; Score 80; DB 2; Length 464;

Best Local Similarity 27.5%; Pred. No. 14;

Matches 36; Conservative 17; Mismatches 46; Indels 32; Gaps 7;

QY 20 ETDVMEALLRVKSSRLAMLRALAGMCHRVLPCTGASAIATVTPKG-ASMKLK--- 75

DB 285 EDYPLGRRLFLYDKGKNPWAQALV-----RFAQGPQGAI---VTRSGFVAQKIQAVQ 336

QY 76 -PPRPOSTKSPLELRLSRKIREMNKTIISOESARVNHRLPEGHPLLEKRA-----EYF 126

DB 337 IAPRPQ--MFAEYRKLAEQARLT-----VNFQFGSALLDNKALLDVQRLDYL 385

QY 127 RHLRLSKSQV 137

DB 386 RQNRKQERTV 396

RESULT 8

T49878

respiratory burst oxidase protein A - Arabidopsis thaliana

N:Alternate names: protein T211.100

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49878

R:Bavan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le

submitted to the Protein Sequence Database, April 2000

A:Reference number: 224493

A:Accession: T49878

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-902 <BEV>

A:Cross-references: EMBL:AL163912; GSPDB:GN00063; ATSP:T211.100

A:Experimental source: cultivar Columbia; BAC clone T211

C:Genetics:

A:Gene: ATSP:T211.100

A:Map position: 5

A:Introns: 180/1; 232/2; 248/3; 286/3; 428/3; 557/3; 589/3; 628/2; 662/3; 687/2; 867/1

Query Match

Best Local Similarity 25.2%; Pred. No. 30;

Matches 37; Conservative 22; Mismatches 42; Indels 46; Gaps 7;

QY 3 STSTTNFVAENRPTFGTDFV-----MREALLRV-KSERLA 39

DB 31 NVATTSTNYGEDEFPYVEITLIDHDSVSVYGLKSPNHRGAGSNYEDQSLLRQGRSGRSNS 90

QY 40 MLRALAGMCHRVLPCTGASAIATVTPKGASMKLPPRPQSTK---SPLELRLSRK-IR 95

DB 91 VLKRLASSV-----STGTRFVASSVSSSSAR---KPPRLQAKLRKSRRAELAKGLK 141

RESULT 11

S42957
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42957
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: in vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Accession: S42957
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30618; NID:G459478; PIDN:CAA83095.1; PID:G459479
C:Superfamily: AIDS vif protein

Query Match 11.2%; Score 79; DB 2; Length 192;
Best Local Similarity 27.9%; Pred. No. 6;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLALAG-----MCGRHVLPGTGASAIATATVTPKGASM 72
DB 112 FDCSESIR-----KAIQGVSPCEVQAGHNKVGSLQYLALALITPK---- 157
QY 73 KKKPPRPOSTKSPELRSKIRENNKTIQSARVNHRLPEGH 116
DB 158 KIKPPLPSVTKLTEDR-----WNKPQTKGRGSHTM-NGH 192

RESULT 12

T17272
hypothetical protein DKFP434B0435.1 - human
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C:Accession: T17272; T46451; A36881
R:Pousta, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18723
A:Accession: T17272
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1780 <POU>
A:Cross-references: EMBL:AL117496
A:Experimental source: adult testis; clone DKFP434B0435
R:Angorge, W.; Winkler, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23028
A:Accession: T46451
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 575-1136, 'C', 1138-1608, 'K', 1610-1780 <AAA>
A:Cross-references: EMBL:AL137322; clone DKFP434I152
R:Westendorf, J.M.; Rao, P.N.; Gerace, L.
Proc. Natl. Acad. Sci. U.S.A. 91, 714-718, 1994
A:Title: Cloning of cDNAs for M-phase phosphoproteins recognized by the MP2 monoclonal
A:Reference number: A36881; MUID:94119956; PMID:8290587
A:Accession: A36881
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1215-1261, 'E', 1263-1418, 'S', 1420-1608, 'K', 1610-1780 <WES>
A:Cross-references: GB:L16782; NID:G292328; PIDN:AAC37542.1; PID:G292329
C:Genetics:
A>Note: DKFP434B0435.1; DKFP434I152.1
C:Keywords: phosphoprotein

Query Match 11.2%; Score 79; DB 2; Length 1780;
Best Local Similarity 21.3%; Pred. No. 83;
Matches 32; Conservative 27; Mismatches 77; Indels 14; Gaps 2;
QY 2 ESTSTTNFVAENRRPTFGTDFVMREALLRVKSSERLAMLALAGMCGHVRVLPOTGASAI 61

DB 604 EYTOFTQYWAQREADFKETLLQERE-IILENAERRLAIFKDLVGKCDTREAAXDICAT 662
QY 62 AATVTPKGASMKLKPDPPOSTKSPELRSKIRENNKTIQSARV----- 108
DB 663 KYETEATACLEKFNQIKAEIAKATKGLIKTEELKKEGNESSDLSIQLETSNKKIITQ 722
QY 109 NURLPBGHPLEKRAEYFRHLRLSLKSGQVN 138
DB 723 NQRIKELINIIOQKEDTINEFONLAKSHMEN 752
RESULT 13
S61809
M-like protein enn precursor - Streptococcus pyogenes (serotype M46) (fragment)
C:Species: Streptococcus pyogenes
A:Variety: serotype M46
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
C:Accession: S61809
R:Whitmore, A.M.; Kapur, V.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 15, 1039-1048, 1995
A:Title: Molecular population genetic analysis of the enn subdivision of group A strept
A:Reference number: S61799; MUID:95349390; PMID:7623660
A:Accession: S61809
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-92 <WHA>
A:Cross-references: EMBL:U20825; NID:G687746; PIDN:AAA87906.1; PID:G687747
A:Experimental source: NCTC 8230; serotype M46
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C:Genetics:
A:Gene: enn
C:Superfamily: M5 protein
C:Keywords: cell wall; surface antigen; virulence
Query Match 11.1%; Score 78.5; DB 2; Length 92;
Best Local Similarity 32.9%; Pred. No. 2.8;
Matches 26; Conservative 15; Mismatches 29; Indels 9; Gaps 3;
QY 55 GTGASAIATVTPKG-----ASMKLK-PPRQST----KSPBELRSKIRENNKTIQS 105
DB 9 GTASVAVALTVLGAGFANQTTKAEVEPRPLATGTGKSRKLDLYNLHDSNLSQVLEK 68
QY 106 ARVNHLPEGHPLLEKRAE 124
DB 69 ALLDKLELEKEKKAEE 87
RESULT 14
F90693
mechanosensitive channel protein [imported] - Escherichia coli (strain O157:H7, substra
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: F90693
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90693
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1120 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA33941.1; PID:G13359975; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs0518
Query Match 11.1%; Score 78.5; DB 2; Length 1120;
Best Local Similarity 24.0%; Pred. No. 53;
Matches 24; Conservative 16; Mismatches 41; Indels 19; Gaps 2;
QY 4 TSTTTNFVAENRRPTFGTDFVMREALLRVKSSERLAMLALAGMCGHVRVLPOTGASAI 63

QY 4 TSTTNFVAENPTTGCTFDVNR EALLRVKSSERLAMLALAGMCGHRVLPGTGA SAIAA 63
 ||||| :
 Db 997 TDTTTLRLVGAYGSDLEKVKR VLLKAATPRVM-----HEPMPVFVTFAG A 1047

QY 64 TVTPKGASKMLAPRPQSTKS PELRELSKIREMNKTISQ 103
 ||||| :
 Db 1048 STLDHELRLIYVR-----ELDRSRTVDLNR TIQ 1077

RESULT 17
D96547
hypothetical protein F23H24.12 imported! - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96547
R:Authors: Saltsberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; D.
ansen, N.P.; Hughes, B.; Huiznar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96547
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <STO>
A:Cross-references: GB:AE005173; NID:gl1128410; PIDN:AAG31212.1; GSPDB:GN00141
C:Genetics:
A:Gene: F23H24.12
A:Map position: 1

Query Match 11.0%; Score 78; DB 2; Length 171;
Best Local Similarity 28.4%; Pred.No. 6.4;
Matches 25; Conservative 13; Mismatches 18; Indels 32; Gaps 4;

QY 81 STKSPELRSKIREMNKTIS---CESAVNHRLPEGHP----- 117
Db 7 TSSTFEFLCELRITQNNDIQNLVRENAQLNH--PIGRYFDAIEVRKKLNDRMKLQ 64

QY 118 -LLEKRAEYFR-----HLRSLKSQGVN 138
Db 65 ELYEKKEVMKEKETPHLKSRLRKQVAN 92

RESULT 18
S42959
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: Human immunodeficiency virus type 1, HIV-1
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42959
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Accession: S42959
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <MIE>
A:Cross-references: EMBU:D30620; NID:g459482; PIDN:CAA83097.1; PID:g459483
C:Superfamily: AIDS vif protein

Query Match 11.0%; Score 78; DB 2; Length 192;
Best Local Similarity 30.5%; Pred.No. 7.4;
Matches 29; Conservative 10; Mismatches 42; Indels 14; Gaps 4;

QY 22 FDVNR EALLRVKSSERLAMLALAGMCGHRVLPGTGA SAIAATVTPKGASKUKLP RPQS 81
Db 112 FDCFFSSAISALTVIGIVSPRC-EYGAGHNKVGSLQYLAAALITPK----KIKPPJFSV 166

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Qy 82 TKSPRLRLSRKIREMNTKTSQESARVNHRLPEGH 116
Db 167 TKLTEDR-----WNKPKQTKGRGSHTM-TGH 192

RESULT 19
72855 hypothetical protein APE0673 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C/Accession: F72655
R/Kawababayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: F72655
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-686 <KAW>
A/Cross-references: DDBJ:AP000060; NID:g5104188; PID:d1043432; PID:g510
A/Experimental source: strain K1
C/Genetics:
A/Gene: APE0673

Query Match 11.0%; Score 78; DB 2; Length 686;
Best Local Similarity 25.4%; Pred. No. 33;
Matches 30; Conservative 15; Mismatches 39; Indels 34; Gaps 4;

Qy 49 GHRVLPGTGASAIATVTPKGASMKLPPRQSTKSPRLRLSRK-----REM 97
Db 175 GLAAVEASGGVVAVAPVKGALSKI-----SPEILRLNLSIYTPPEGVGGSPREA 225

Qy 98 NKTISQESARVNHRLPEGHPLLEK-----ABY-----FRLRLSLKSQGVNRLI 141
Db 226 MEYIRGEKARGLRLVSIQEMASERLGAFFYTWAFENIKFLVLTSLRGETRIV 283

RESULT 20
A45339 outer capsid protein VP5 - Broadhaven virus
C/Species: Broadhaven virus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C/Accession: A45339
R/Moss, S.R.; Fukusho, A.; Nuttall, P.A.
Virology 179, 482-484, 1990
A/Title: RNA segment 5 of Broadhaven virus, a tick-borne orbivirus, shows sequence homol
A/Reference number: A45339; MUID:91021056; PMID:2171220
A/Accession: A45339
A/Molecule type: genomic RNA
A/Residues: 1-480 <MOS>
A/Cross-references: GB:M58030; NID:g210813; PIDN:AAA42802.1; PID:g210814
C/Genetics:
A/Map position: segment 5
C/Superfamily: bluetongue virus outer capsid protein VP5
C/Keywords: capsid protein; coat protein; glycoprotein
F:122,201/Binding site: carbohydrate (Asn) #status predicted

Query Match 10.9%; Score 77.5; DB 1; Length 480;
Best Local Similarity 24.6%; Pred. No. 24;
Matches 33; Conservative 22; Mismatches 60; Indels 19; Gaps 5;

Qy 14 NRPTFGFTDYMREALLRVKSSERLAMLRLAGMCGHRVLPGT--GASATAATVTPKGAS 71
Db 15 NRIGSGITRAARSDDTKRIPSAAGRAVERVAASIGQRAIAGVVEGATAALTGESVGES 74

Qy 72 MK-----LKPRPOSTKSPRLRLSRKIREMNTKTSQESARVNHRLPEGHPLLEK 122
Db 75 VKRAVLNVAGVHTQVDPDLPNVEI-ETQAKRLDLANKREEAQIRH-----NKSMLQKE 129

Qy 123 AEYF---RHLRLSLK 133
Db 158 KIKPPLPSVTKLTEDR-----WNKPKQTKGRGSHTM-NGH 192

Db 130 AQILGEVOHLMTVQ 143

RESULT 21
ASLJS3
vif protein - human immunodeficiency virus type 1
N/Alternate names: orf-Q protein; sor protein
C/Species: human immunodeficiency virus type 1, HIV-1
C/Date: 17-May-1985 #sequence_revision 31-Mar-1993 #text_change 16-Jul-1999
C/Accession: A04002; A36757; A36756; A36765; S42971
R/Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A/Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of
A/Reference number: A94093; MUID:86177573; PMID:3008154
A/Accession: A04002
A/Molecule type: DNA
A/Residues: 1-192 <ARY>
A/Cross-references: GB:M11840; NID:g328453; PIDN:AAA44997.1; PID:g328454
A/Experimental source: isolate HTLV-III, 12
R/Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dor
nberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A/Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A/Reference number: A93353; MUID:85111123; PMID:2578615
A/Accession: A36757
A/Molecule type: DNA
A/Residues: 1-192 <RAT>
A/Cross-references: GB:M15654; NID:g326383; PIDN:AAA44202.1; PID:g326389
A/Experimental source: isolate HTLV-III, BH10
R/Hair-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A/Title: Nucleotide sequence of the AIDS virus, LAV.
A/Reference number: A90866; MUID:85099333; PMID:2981635
A/Accession: A36756
A/Molecule type: DNA
A/Residues: 1-192 <RAI>
A/Cross-references: GB:K02013; NID:g326417; PIDN:AA859748.1; PID:g326421
A/Experimental source: isolate LAV-1a
R/Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A/Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A/Reference number: A93355; MUID:85111157; PMID:2982104
A/Accession: A36765
A/Molecule type: DNA
A/Residues: 1-192 <MUE>
A/Cross-references: GB:X01762
A/Experimental source: isolate LV
R/Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A/Description: In vivo genetic variability of the HIV-1 gene.
A/Reference number: S42940
A/Accession: S42971
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-192 <WIE>
A/Cross-references: EMBL:Z30632; NID:g459506; PIDN:CAA83109.1; PID:g459507
C/Genetics:
A/Gene: vif
C/Superfamily: AIDS vif protein
C/Keywords: AIDS; immunodeficiency

Query Match 10.9%; Score 77; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDMREALLRVKSSERLAMLRLAG-----MCGHRVLPGTGASATAATVTPKGAS 72
Db 112 FCFDSAIR-----KALLGHVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KKKPRPOSTKSPRLRLSRKIREMNTKTSQESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTEDR-----WNKPKQTKGRGSHTM-NGH 192

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RESULT 22
ASLONA
vif protein - human immunodeficiency virus type 1 (isolate NIT-A)
N:Alternate names: orf-Q protein; sor protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Jan-1997
E:Sakai, K.; Ma, X.; Gordienko, I.; Volsky, D.J.
J. Virol. 65, 5765-5773, 1991
A:Title: Recombinational analysis of a natural noncytopathic human immunodeficiency virus
A:Reference number: A41308; MUID:92015467; PMID:1920615
A:Accession: A41308
A:Molecule type: DNA
A:Residues: 1-192 <SAK>
C:Genetics:
A:Gene: vif
A:Superfamily: AIDS vif protein
C:Keywords: AIDS; immunodeficiency

Query Match 10.9%; Score 77; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

QY 73 KLPKPPQSTKSPELRELSRKIREMNKTIQESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTEDR-----WNKPQTKGHRGHTM-NGH 192

RESULT 23
S42964
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42964
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30625; NID:g459492; PIDN:CAA83102.1; PID:g459493
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

QY 73 KLPKPPQSTKSPELRELSRKIREMNKTIQESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTEDR-----WNKPQTKGHRGHTM-NGH 192

RESULT 24
S42960
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42960
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
```

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A:Reference number: S42940
A:Accession: S42960
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30621; NID:g459484; PIDN:CAA83098.1; PID:g459485
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

QY 73 KLPKPPQSTKSPELRELSRKIREMNKTIQESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTEDR-----WNKPQTKGHRGHTM-NGH 192

RESULT 25
S42940
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C:Accession: S42940
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30601; NID:g459446; PIDN:CAA83078.1; PID:g459447
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 30.5%; Pred. No. 9.1;
Matches 29; Conservative 9; Mismatches 43; Indels 14; Gaps 4;

QY 22 FDMREALLRVKSSERLAMLRLALAGMCGHRVLPGTGASAIATVTPKGASKMLKPPRPOS 81
Db 112 FDCFSESAIRKAIVGLVNPVRC-EYLAGHNKVGSLQYLALALITPK----KIKPPLPSV 166

QY 82 TKSPELRELSRKIREMNKTIQESARVNHRLPEGH 116
Db 167 RKLTEDR-----WNKPQTKGHRGHTM-NGH 192

RESULT 26
S42946
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42946
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30607; NID:g459458; PIDN:CAA83084.1; PID:g459459
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
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Db 112 FDCSDSAIR-----KALLGHIVSPCEYQAGNKRKVGSLQYLALAAALITPK----- 157
Qy 73 KKKPPRPOSTKSPRLSRKIRENNKTIQSASRVNHLRPEGH 116
Db 158 KKKPPRPOSTKSPRLSRKIRENNKTIQSASRVNHLRPEGH 192
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing en-
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: E95966
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC49397.1; PID:G15140883; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, P.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
A:Genetics:
C:Gene: SMb21557
A:Genome: plasmid

Query Match 10.7%; Score 76; DB 2; Length 325;
Best Local Similarity 26.6%; Pred. No. 21;
Matches 33; Conservative 11; Mismatches 42; Indels 38; Gaps 5;

Qy 37 RLAMRLAGMCHRVLPOTGASAI-----AATVTPKGASM 72
Db 115 RCPYFRLDAPCNKRV-PGSGCSAIDGLNAGHAILGTSEHCVAITHPSDLAVSLVALGANL 173
Qy 73 KKKPPRPOSTKSPRLSRKIRENNKTIQSASRVNHLRPEGHPLLE---KRAEYFRHL 129
Db 174 SLKGPAGERTIPVE--ELFR-----LPSTPHLEHTLEPGELIVEVHPNGPYARKA 223
Qy 130 RSLK 133
Db 224 RYLK 227

RESULT 30
E82992
Probable FAD-dependent monooxygenase PA5221 [imported] - Pseudomonas aeruginosa (strain
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E82992
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; E
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E82992
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: GB:AE004935; GB:AE004935; PIDN:G9951526; PIDN:AAG08606.1; GSPDB:GN00
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5221
C:Superfamily: ubiH protein

Query Match 10.7%; Score 76; DB 2; Length 405;
Best Local Similarity 23.2%; Pred. No. 27;
Matches 23; Conservative 19; Mismatches 39; Indels 18; Gaps 3;

Qy 45 AGMCGHRV---LPGTGASAIATVTPKGASMKLKKPPRPOSTKSPRLSRKIRENNKTI 101
Db 115 RCPYFRLDAPCNKRV-PGSGCSAIDGLNAGHAILGTSEHCVAITHPSDLAVSLVALGANL 173
Qy 45 AGMCGHRV---LPGTGASAIATVTPKGASMKLKKPPRPOSTKSPRLSRKIRENNKTI 101
Db 115 RCPYFRLDAPCNKRV-PGSGCSAIDGLNAGHAILGTSEHCVAITHPSDLAVSLVALGANL 173

Db 112 FDCSDSAIR-----KALLGHIVSPCEYQAGNKRKVGSLQYLALAAALITPK----- 157
Qy 73 KKKPPRPOSTKSPRLSRKIRENNKTIQSASRVNHLRPEGH 116
Db 158 KKKPPRPOSTKSPRLSRKIRENNKTIQSASRVNHLRPEGH 192
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing en-
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: E95966
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC49397.1; PID:G15140883; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, P.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
A:Genetics:
C:Gene: SMb21557
A:Genome: plasmid

Query Match 10.9%; Score 77; DB 2; Length 889;
Best Local Similarity 26.8%; Pred. No. 55;
Matches 26; Conservative 17; Mismatches 46; Indels 8; Gaps 1;

Qy 20 ETDVMEALLRVKSSERLAMLRLAGMCHRVLPOTGASAIATVTPKGASMKLKKPPR 79
Db 744 ESKFLTRIPRGENTSADTLAALASTDPFVKRIIPVEGIEHTSIDLVKVGAGMEPEAPP 803
Qy 80 QSTKSPRLSRKIRENNKTIQSASRVNHLRPEGHPLLE---KRAEYFRHL 129
Db 804 QLESLRQRQRQVRKSRKIRENNKTIQSASRVNHLRPEGHPLLE---KRAEYFRHL 129

RESULT 28
S42977
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1_HIV-1
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42977
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Accession: S42977
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:230639; NID:G459520; PIDN:CAA83116.1; PID:G459521
C:Superfamily: AIDS vif protein

Query Match 10.7%; Score 76; DB 2; Length 192;
Best Local Similarity 28.0%; Pred. No. 11;
Matches 30; Conservative 11; Mismatches 28; Indels 38; Gaps 6;

Qy 22 FDMVMEALLRVKSSERLAMLRLAGMCHRVLPOTGASAIATVTPKGASMKLKKPPR 79
Db 112 FDCSDSAIR-----KALLGHIVSPCEYQAGNKRKVGSLQYLALAAALITPK- 157
Qy 70 ASMKLKKPPRPOSTKSPRLSRKIRENNKTIQSASRVNHLRPEGH 116
Db 158 ---KINPLPSIKKLTEDR-----WNKPKTKGHRGSHTM-NGH 192

RESULT 29
```

```
Db 10 AGMVGSALALALEGSGUEVLV-----DGGSLDVAPFKPEAYEPRV-----SAL 54
QY 102 SQESARNVHRLPEGHPLLEKRAEYFRHLRLSLKSGQVNL 140
Db 55 SEASRRILQRLHWDGIVARAEFYREMQVWDGSGTGRI 93

RESULT 31
G70522
C:Species: Mycobacterium tuberculosis (strain H37RV)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: G70522
R;Cole, S.R.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70522
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-408 <COL>
A:Cross-references: GB:297188; GB:AL123456; NID:93261805; PIDN:CAB10011.1; PID:g2224818
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3827c
C:Superfamily: hypothetical protein bl432

Query Match 10.7%; Score 76; DB 2; Length 408;
Best Local Similarity 30.6%; Pred. No. 27;
Matches 33; Conservative 11; Mismatches 44; Indels 20; Gaps 5;

QY 49 CHRVLPOTGASATAATVTPKGASMKLP-PPPOSTKSPELR-----ELSRKIREM 97
Db 218 GSRVGVGVVRLATVANAGVLEEVNPRPLDTALKELYASRARSCTKGSRRYR 277
QY 98 NKTIQSASRVN-----HRLPEGHPLLEKRAEYFRHL--RSLKSGQVNR 139
Db 278 TTEISRLHRRVNDVRTHHL---HVLITRLAQTHGVVEGLDAGMLR 322

RESULT 32
I49603
transcription regulator - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49603
R;Galera, P.; Musso, M.; Ducey, P.; Karsenty, G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9372-9376, 1994
A:Title: c-Krox, a transcriptional regulator of type I collagen gene expression, is predicted to be a homeodomain protein
A:Reference number: I49603; MUID:95023913; PMID:793772
A:Accession: I49603
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-427 <RES>
A:Cross-references: GB:L35307; NID:G529399; PIDN:AAA61956.1; PID:G529400
C:Genetics:
A:Gene: c-Krox

Query Match 10.7%; Score 76; DB 2; Length 427;
Best Local Similarity 25.0%; Pred. No. 29;
Matches 35; Conservative 15; Mismatches 50; Indels 40; Gaps 7;

QY 32 VKSSERLAMLALAGMCHRVLPOTGASA-----IAATVT-----P 67
Db 4 VLQAAALLLEIPCVAIAC-MEILQSGLEAPSPDEDDCERARQVLEAFATATTASTSGMP 62
QY 68 KG-----ASKMLKPPRQSTKSPRLRELSKIREMNTISQ-ESARNVHRLPEG-----HP 117
Db 63 NGEDSPQVPLLEPPP-----PPRPRVARSRRPRKAFLOTQGARANHLLVPEAPTVLTHP 117

QY 118 LLEKRAEYFRHLRLSLKSGQV 137
Db 118 LTYEEEMVGRNLGSGGSL 137

RESULT 33
G75403
DNA topoisomerase I - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: G75403
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75403
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1021 <WHI>
A:Cross-references: GB:AE001983; GB:AE000513; NID:G6459123; PIDN:AAF10943.1; PID:G64591
A:Experimental source: strain R1
C:Genetics:
A:Gene: BR1374
A:Map position: 1
C:Superfamily: bacterial type I DNA topoisomerase

Query Match 10.7%; Score 76; DB 2; Length 1021;
Best Local Similarity 28.2%; Pred. No. 80;
Matches 37; Conservative 20; Mismatches 40; Indels 34; Gaps 7;

QY 28 ALLRVKSSERLAMLALAGMCHRVLPOTG-----ASAIATVTPKGASMKL----- 74
Db 267 ARLTEVQGERLAAGKDFDLTG-QLRPGAGVRLGAEALAISEGLKQTLKVLTAEEKP 325
QY 75 ---KPPRQSTKSPRLRELSKIREMNTISOESARNVHRLPEGHPLLEKRAEYFRHLR- 130
Db 326 FTSRPPAPFITSILO-QEGSRKLR---MSAQTMTRTAQRLYEG-----GYITYMRT 372
QY 131 ---SLKSGQVNR 138
Db 373 DSTNLSSBAVN 383

RESULT 34
F97169
static acid synthase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: F97169
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C. acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: F97169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK80145.1; PID:g15025183; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2187
C:Superfamily: Streptococcus agalactiae capsular polysaccharide biosynthesis protein cp

Query Match 10.7%; Score 75.5; DB 2; Length 350;
Best Local Similarity 27.1%; Pred. No. 25;
Matches 32; Conservative 14; Mismatches 45; Indels 27; Gaps 4;

QY 20 ETFDVMREALLRVKSSERLAMLALAGMCHRV--LPOTGASAIATVTPKGASMKLKPP 77
Db 200 KTIPTMREA-----FNCSVGLSDHTMGYSVATAAVALGATVIEGHFTLKRS 247
```

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: G75302
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-606 <WHI>
 A:Cross-references: GB:AE002053; GB:AE000513; NID:G459999; PIDN:AAF11749.1; PID:G64500
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2200
 A:Map position: 1

Query Match 10.6%; Score 75; DB 2; Length 606;
 Best Local Similarity 26.0%; Pred. No. 53;
 Matches 33; Conservative 20; Mismatches 58; Indels 16; Gaps 5;

QY 13 ENRP-----TGCTFDVNRALLRVKSRERLALAG-MGHRVLPCTGASIAATVT 66
 DB 81 EQRPQFPQFVFRQRTGLRAKQVQVKEQPRQPAAGGVVGVQVHPVVGQAAP-R 139
 QY 67 PKGASMKLPPRPOSTK---SPELRELSRKIREMKNKTIQSARVNHRLPEGHPLLEKRA 123
 DB 140 PRAQRRRLPAPVAARLVPCPQRQQTAGERQLVPLPCPHRVQHARPGEDVALN--- 196
 QY 124 EYFHLR 130
 DB 197 ---RHVR 200

RESULT 38
 A48467
 myosin heavy chain - nematode (Brugia malayi) (fragment)
 C:Species: Brugia malayi
 C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
 C:Accession: A48467
 R:Dissanayake, S.; Xu, M.; Plessens, W.F.
 Mol. Biochem. Parasitol. 56, 349-351, 1992
 A:Title: Myosin heavy chain is a dominant parasite antigen recognized by antibodies in
 A:Reference number: A48467; MUID:93133225; PMID:1484558
 A:Accession: A48467
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-1313 <DIS>
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:122784, NCBI:122786)
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP

Query Match 10.6%; Score 75; DB 2; Length 1313;
 Best Local Similarity 27.0%; Pred. No. 1.3e+02;
 Matches 20; Conservative 15; Mismatches 33; Indels 6; Gaps 1;

QY 73 KLPKPRPOSTKSPELRELSRKIREMKNKTIQSARVNHRLPEGHPLLEKRAEYFRHLRSL 132
 DB 199 KIKPKMLKCGEGEIEKNQKIKELKENIANEAKELSENSTKLLERNNVFNLEAA 258
 QY 133 KSQ-----GVNRL 140
 DB 259 KAQLSDVDDRLNRL 272

RESULT 39
 A45627
 myosin heavy chain [similarity] - nematode (Brugia malayi)
 C:Species: Brugia malayi
 C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
 C:Accession: A45627; B45526
 R:Werner, C.; Rajan, T.V.
 Mol. Biochem. Parasitol. 50, 261-268, 1992
 A:Title: Characterization of a myosin heavy chain gene from Brugia malayi.

78 RPOSTKSPELRELS---RKIREMKNKTIQSARVNHRLPEGHPLLEKRAEYFRHLRSL 132
 DB 248 GPDSARSMBEPESAMVKSIREVEKALGVY-----YELTEKQKNSQHSRSL 295

RESULT 35
 S43000
 viral infectivity factor vif - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
 C:Accession: S43000
 R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
 submitted to the EMBL Data Library, March 1994
 A:Description: In vivo genetic variability of the HIV-1 gene.
 A:Reference number: S42940
 A:Accession: S43000
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-192 <WIE>
 A:Cross-references: EMBL:Z30691; NID:G459619; PIDN:CAA83171.1; PID:G459620
 C:Superfamily: AIDS vif protein

Query Match 10.6%; Score 75; DB 2; Length 192;
 Best Local Similarity 27.1%; Pred. No. 14;
 Matches 29; Conservative 9; Mismatches 31; Indels 38; Gaps 5;

QY 22 FDMREALLRVKSSERLALAGMCHRVLP-----GTGASATAATVTPKG 69
 DB 112 FDCFSASIR-----QALGHRVSPCEYRAGHNKVGSLQYLALITALITPK- 157
 QY 70 ASMKLPPRPOSTKSPELRELSRKIREMKNKTIQSARVNHRLPEGH 116
 DB 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 36
 S42965
 viral infectivity factor vif - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
 C:Accession: S42965
 R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
 submitted to the EMBL Data Library, March 1994
 A:Description: In vivo genetic variability of the HIV-1 gene.
 A:Reference number: S42940
 A:Accession: S42965
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-192 <WIE>
 A:Cross-references: EMBL:Z30626; NID:G459494; PIDN:CAA83103.1; PID:G459495
 C:Superfamily: AIDS vif protein

Query Match 10.6%; Score 75; DB 2; Length 192;
 Best Local Similarity 29.0%; Pred. No. 14;
 Matches 31; Conservative 9; Mismatches 29; Indels 38; Gaps 6;

QY 22 FDMREALLRVKSSERLALAGMCHRVLP-----TGA---SATAATVTPKG 69
 DB 112 FDCFSASIR-----NALGHRVSPCEYRAGHNKVGSLQYLALITALITPK- 157
 QY 70 ASMKLPPRPOSTKSPELRELSRKIREMKNKTIQSARVNHRLPEGH 116
 DB 158 ---KIKPPLPSVAKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 37
 G75302
 orotidine 5'-phosphate decarboxylase - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: G75302
 R:White, C.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:30 ; Search time 37 Seconds

(without alignments)
179,210 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 708

Sequence: 1 MESTSTTNFVAENRPTFGE.....RAEYFRHLRLSKQGVNRLI 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	11.6	700	1 TRDN CANFA	P82179 canis famil
2	78.5	11.1	1120	1 KEPA_ECOLI	P77338 escherichia
3	78	11.0	686	1 VATI_AERPE	Q9yea0 aeropyrum p
4	77.5	10.9	480	1 VP5_ERD	P21230 broadhaven
5	77	10.9	192	1 VIF_HV1B1	P31401 human immun
6	77	10.9	192	1 VIF_HV1A	P31820 human immun
7	76	10.7	192	1 VIF_HV1B5	P04598 human immun
8	74.5	10.5	400	1 DH12_RAT	P50233 rattus norv
9	74	10.5	662	1 TLPB_BACSU	P39217 bacillus nor
10	74	10.5	908	1 VP2_ERD	P35934 broadhaven
11	73.5	10.4	429	1 VIOC_CHRVO	Q98309 chromobacte
12	73.5	10.4	437	1 YGY3_HALSQ	P21561 haloterrax s
13	73.5	10.4	1187	1 PTNE_HUMAN	Q15678 homo sapien
14	73	10.3	109	1 VIF_HV1C	P05899 human immun
15	73	10.3	666	1 FLID_VIBCH	Q9kg63 vibrio chol
16	72	10.2	642	1 PHSA_STPAT	Q53692 streptomyce
17	72	10.2	1805	1 HNW2_MYCGE	P47460 mycoplasma
18	72	10.2	3259	1 GRAN_HUMAN	Q14789 homo sapien
19	71.5	10.1	212	1 NUIM_BOVIN	P42028 bos taurus
20	71.5	10.1	392	1 PGK_NEIMB	Q9jws8 neisseria m
21	71.5	10.1	392	1 PGK_NEIMB	Q9klr0 neisseria m
22	71.5	10.1	559	1 Y876_MYCTU	Q10564 mycobacteri
23	71.5	10.1	732	1 YN8K_YEAST	Q03254 saccharomyc
24	71.5	10.1	748	1 CIAT_HUMAN	P28329 homo sapien
25	71.5	10.1	2564	1 SFCO_HUMAN	Q9h254 homo sapien
26	71	10.0	192	1 VIF_HV1RH	P05900 human immun
27	71	10.0	211	1 HIT_PIG	P06348 sus scrofa
28	71	10.0	377	1 HSF7_ARATH	Q9t0d3 arabidopsis
29	71	10.0	411	1 AFGM_PYRAB	Q9v2m6 pyrococcus
30	71	10.0	411	1 AFGM_PYRUF	P58814 pyrococcus
31	71	10.0	1061	1 RNE_ECOLI	P21513 escherichia
32	71	10.0	1189	1 PTNE_MOUSE	Q82130 mus musculu
33	70.5	10.0	570	1 ZDS_FAIZE	Q9ztp4 zea mays (m

ALIGNMENTS

RESULT 1

ID	TRDN CANFA	STANDARD:	PRT:	700 AA.
AC	P82179:			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Triadin.			
GN	TRDN.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RC	TISSUE=Heart, and Skeletal muscle;			
RX	MEDLINE=99428545; PubMed=10497235;			
RA	Kobayashi Y.M., Jones L.R.;			
RT	"Identification of triadin 1 as the predominant triadin isoform expressed in mammalian myocardium";			
RL	J. Biol. Chem. 274:28660-28668(1999).			
CC	FUNCTION: MAY BE INVOLVED IN ANCHORING CALSEQUESTIN TO THE JUNCTIONAL SARCOPLASMIC RETICULUM AND ALLOWING ITS FUNCTIONAL COUPLING WITH THE RYANODINE RECEPTOR (BY SIMILARITY).			
CC	COUPLING WITH THE RYANODINE RECEPTOR (BY SIMILARITY).			
CC	SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic reticulum.			
CC	ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Name=Skeletal;			
CC	ISOID=P82179-1; Sequences=Displayed;			
CC	Name=Cardiac 1;			
CC	ISOID=P82179-2; Sequences=VSP_004001, VSP_004002;			
CC	Name=Cardiac 3;			
CC	ISOID=P82179-3; Sequences=VSP_004003, VSP_004004;			
CC	TISSUE SPECIFICITY: SKELETAL AND CARDIAC MUSCLE.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			

DR	EMBL; AF165916; AAF00222.1; ..			
DR	EMBL; AF165915; AAF00221.1; ..			
DR	EMBL; AF165917; AAF00223.1; ..			
DR	Transmembrane; Sarcoplasmic reticulum; Glycoprotein; Alternative splicing.			
KW	INIT_MET 0 0			
FT	DOMAIN 1 46			
FT	TRANSMEM 47 67			
FT	DOMAIN 68 700			
FT	CARBOHYD 74 74			
FT	CARBOHYD 616 616			
FT	VARSPLIC 257 277			

DQYAFRCYMDMFVHGDLRPG -> GKHSSEVAGGSKRTLG (POTENTIAL).

```

FT FT KKQIQ (in isoform Cardiac 1).
FT FT /FTID=VSP 004001.
FT FT Missing (in isoform Cardiac 1).
FT FT VARSPLIC 278 700
FT FT /FTID=VSP 004002.
FT FT Missing (in isoform Cardiac 1).
FT FT VARSPLIC 466 466
FT FT E -> EPIGKSVKVPGLSKE (in isoform Cardiac 3).
FT FT /FTID=VSP 004003.
FT FT EKVVKQVRAATEKAAIEKTVKPKAKAHOEKESPTIKTD
FT FT KKPTSKETPEVTES -> GILQVVPVNLCLPLVQFQDE
FT FT ELNVESKVRMRHVLVSHPTSRISPLVISTCT (in isoform Cardiac 3).
FT FT /FTID=VSP 004004.
FT FT SEQUENCE 700 AA; 78152 MW; F033E3AA1BEE0C56 CRC64;
FT FT
FT FT Query Match 11.6%; Score 82; DB 1; Length 700;
FT FT Best Local Similarity 27.4%; Pred. No. 7.1;
FT FT Matches 26; Conservative 15; Mismatches 34; Indels 20; Gaps 2;
FT FT
QY 56 TGASATAAATVTPKA-----SMKLKPPRPOSTKSPELRELSRKIRENMKTIQSE 104
DB 534 TEKAAIEKTVKPKAKAHOEKESPTIKTDKPKPTSKETFEVTESGKKKIEKSEKSE 593
QY 105 SARVNHRLPEGHLLLEKRAEYFPHRLSLKSGQVNR 139
DB 594 KAEMKEL-----KEEKVSTRKESLQSHNVTK 619
QY
DB
RESULT 2
KEFA_ECOLI STANDARD; PRT; 1120 AA.
ID ID KEFA_ECOLI
AC P77336;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium efflux system Kefa (Asefa protein).
GN KEFA OR AEF4 OR B0455.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Jones M.A., McTaggen D., Epstein W., Booth I.R.;
RT "Characterisation of the aefA locus of E.coli.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden W.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[3]
RN [3]
RP SEQUENCE FROM N.A.
RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
RA Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
RA Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[4]
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99219852; PubMed=10202137;
RA Levina N., Totemeyer S., Stokes N.R., Louis P., Jones M.A.,
RA Booth I.R.;
RT "Protection of Escherichia coli cells against extreme turgor by
RT activation of MscS and MscL mechanosensitive channels: identification
RT of genes required for MscS activity.";
RL EMBO J. 18:1730-1737(1999).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE UPF0003 FAMILY.

```

CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE.
CC -!- CATALYTIC ACTIVITY: ATP + H(+)O + H(+) (In) = ADP + phosphate +
CC H(+)(Out).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AP000060; BAA79646.1; --
CC PIR; F72655; F72655.
CC InterPro; IPR002490; V_ATPase_sub116.
CC Pfam; PF01496; V_ATPase_sub_1.
CC KEGG; Hydrolyase; Hydrogen ion transport; Transmembrane; Complete proteome.
CC FT TRANSMEM 173 193 POTENTIAL.
CC FT TRANSMEM 349 369 POTENTIAL.
CC FT TRANSMEM 395 415 POTENTIAL.
CC FT TRANSMEM 465 485 POTENTIAL.
CC FT TRANSMEM 539 559 POTENTIAL.
CC FT TRANSMEM 605 625 POTENTIAL.
CC FT TRANSMEM 627 647 POTENTIAL.
CC SQ SEQUENCE 686 AA; 75133 MW; D90A5D479029D8FB CRC64;

CC Query Match 11.0%; Score 78; DB 1; Length 686;
CC Best Local Similarity 25.4%; Pred. No. 16;
CC Matches 30; Conservative 15; Mismatches 39; Indels 34; Gaps 4;

CC QY 49 GHRVLFGTASAIATVTPKASMLKPPRPOSTKSPRLSLRKH-----REM 97
CC DB 175 GLAAVEAGSGVVAVAVPKGALSKI-----SPEILRLNLSIYTPPEGVGSPREA 225
CC QY 98 NKTISQESARVNHRLPEGHPLLEKR-----AEY-----FHLRLSLKSGVNRLLI 141
CC DB 226 MEYIRGEKARGLRRLVSIQEMASERLGEIAEFTVVTAFENIFKFLVSLRKGTRIV 283

CC RESULT 4
CC VPS_BRD
CC ID -VPS_BRD STANDARD; PRT; 480 AA.
CC AC P21230;
CC DT 01-MAY-1991 (Rel. 18, Created)
CC DT 01-MAY-1991 (Rel. 18, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE Outer capsid protein VPS.
CC GN S5
CC OS Broadhaven virus (BRD).
CC OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
CC OX NCBI_TaxID=10893;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91021056; PubMed=2171220;
CC RA Moss S.R., Fukusho A., Nuttall P.A.;
CC RT "RNA segment 5 of broadhaven virus, a tick-borne orbivirus, shows
CC sequence homology with segment 5 of bluetongue virus.";
CC RL Virology 179:482-484(1990).
CC CC -!- FUNCTION: THE VPS5 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP2)
CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID.
CC -!- SIMILARITY: BELONGS TO THE REOVIRUS VPS5 FAMILY.
CC
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CC
CC EMBL; M58030; AAA42802.1; --

DR PIR; A45339; A45339.
DR InterPro; IPR000145; Orbi_VP5.
DR Pfam; PF00901; Orbi_VP5; I.
DR KW Coat protein.
DR SQ SEQUENCE 480 AA; 52522 MW; 28DFD78B2BE923A1 CRC64;

CC Query Match 10.9%; Score 77.5; DB 1; Length 480;
CC Best Local Similarity 24.6%; Pred. No. 12;
CC Matches 33; Conservative 22; Mismatches 60; Indels 19; Gaps 5;

CC QY 14 NRTFTETFDVMEALLRVKSSERLALAGMCHRVLPGT--GASATAATVTPKGAS 71
CC DB 15 NRIGSGITRAARSDDTKRIPSAAGRAVERVAASEIGQRAIAGVVEGAATAALTGESVGS 74
CC QY 72 MK-----LXPPRPQSTKSPRLSLRSLKIREMKNKTSQESARVNHRLPEGHPLLEKR 122
CC DB 75 VKRAVILNVAGVHQTVPDPLNVEI-ETQAKRELDLANKREEAQIRH-----NKSMLOKE 129
CC QY 123 AEYF---RHLSLK 133
CC DB 130 AQILGEVQHLMTVQ 143

CC RESULT 5
CC VIF_HVIB1
CC ID -VIF_HVIB1 STANDARD; PRT; 192 AA.
CC AC P03401;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
CC DT 01-JUL-1993 (Rel. 26, Last annotation update)
CC DE Virus ion infectivity factor (SOR protein).
CC GN VIF.
CC OS Human immunodeficiency virus type 1 (BR10 isolate) (HIV-1),
CC OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1),
CC OS Human immunodeficiency virus type 1 (Clone 12) (HIV-1),
CC OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1), and
CC OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
CC OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
CC OX NCBI_TaxID=11678, 11686, 11679, 11706, 11700;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Isolate BH10;
CC RX MEDLINE=85111123; PubMed=2578615;
CC RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
CC RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
CC RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
CC RA Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
CC RA Wong-Staal F.;
CC RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
CC RL Nature 313:277-284(1985).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=CLONE 12;
CC RX MEDLINE=86177573; PubMed=3008154;
CC RA Arya S.K., Gallo R.C.;
CC RT "Three novel genes of human T-lymphotropic virus type III: immune
CC reactivity of their products with sera from acquired immune
CC deficiency syndrome patients.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC RN [3]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Isolate BRU;
CC RX MEDLINE=85099333; PubMed=2981635;
CC RA Wain-Hobson S., Sonigo P., Dancs O., Cole S., Alison M.;
CC RT "Nucleotide sequence of the AIDS virus, LAV.";
CC RL Cell 40:9-17(1985).
CC RN [4]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Isolate PV22;
CC RX MEDLINE=85111157; PubMed=2982104;
CC RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
CC RA Capon D.J.;
CC RT "Nucleic acid structure and expression of the human

RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458 (1985).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate HX82;
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
virus."
RL AIDS Res. Hum. Retroviruses 3:57-69 (1987).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC
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CC
CC EMBL; K02083; AAB59868.1; -
CC EMBL; M15654; AAA44202.1; -
CC EMBL; M11840; AAA44997.1; -
CC EMBL; K02013; AAB59748.1; -
CC EMBL; X01762; -; NOT ANNOTATED_CDS.
CC EMBL; K03455; AAB50260.1; -
CC EMBL; A04321; CAA00351.1; -
CC PIR; A04002; ASLJ53.
CC HIV; M11840; VIFSPCV12.
CC HIV; M15654; VIFSBH102.
CC HIV; K02013; VIFSPBRU.
CC HIV; K02083; VIFSPV22.
CC HIV; K03455; VIFSHXB2.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22513 MW; D22589F3955CBE40 CRC64;

Query Match 10.9%; Score 77; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 4.2;
Matches 29; Conservative 32; Indels 32; Gaps 5;

Qy 22 FDVREALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRLSKIRENMKTIQESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 6
VIF_HVINA
ID VIF_HVINA STANDARD; PRT; 192 AA.
AC P31820;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (NIT-A isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36376;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92015467; PubMed=1920615;
RA Sakai K., Ma X., Gordienko I., Volsky D.J.;
RT "Recombinational analysis of a natural nontytopathic human
RT immunodeficiency virus type 1 (HIV-1) isolate: role of the vif gene
RT in HIV-1 infection kinetics and cytopathicity."

Qy 22 FDVREALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRLSKIRENMKTIQESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 7
VIF_HVIB5
ID VIF_HVIB5 STANDARD; PRT; 192 AA.
AC P04598;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.P., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284 (1985).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC
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CC
CC EMBL; K02012; AAA44654.1; -
CC HIV; K02012; VIFSHS.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22520 MW; AC17E169F5354493 CRC64;

Query Match 10.7%; Score 76; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 5.2;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDVREALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRLSKIRENMKTIQESARVNHRLPEGH 116

RL J. Virol. 65:5765-5773 (1991).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC PIR; A41308; ASLJNA.
CC InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22611 MW; 9E45529E2387DE8A CRC64;

Query Match 10.9%; Score 77; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 4.2;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDVREALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRLSKIRENMKTIQESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 7
VIF_HVIB5
ID VIF_HVIB5 STANDARD; PRT; 192 AA.
AC P04598;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.P., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284 (1985).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
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CC
CC EMBL; K02012; AAA44654.1; -
CC HIV; K02012; VIFSHS.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22520 MW; AC17E169F5354493 CRC64;

Query Match 10.7%; Score 76; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 5.2;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDVREALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRLSKIRENMKTIQESARVNHRLPEGH 116

Db 158 KVKPPLPSVTKLTEDR-----WNKPKTKGHRGSHTW-NGH 192

RESULT 8

DH12_RAT STANDARD; PRT; 400 AA.
AC P50233;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Corticosteroid 11-beta-dehydrogenase, isozyme 2 (EC 1.1.1.146) (11-
DH2) (11-beta-hydroxysteroid dehydrogenase type 2) (11-beta-HSD2)
DE (NAD)-dependent 11-beta-hydroxysteroid dehydrogenase).
GN HSD11B2 OR HSD11K.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95377198; PubMed=7643078;
RA Zhou M.-Y., Gomez-Sanchez E.F., Cox D.B., Cosby D.,
RA Gomez-Sanchez C.E.;
RT "Cloning, expression, and tissue distribution of the rat nicotinamide
adenine dinucleotide-dependent 11 beta-hydroxysteroid
dehydrogenase";
RT Endocrinology 136:3729-3734 (1995).
RL
CC -1- FUNCTION: Catalyzes the conversion of cortisol to the inactive
metabolic cortisone. Modulates intracellular glucocorticoid
levels, thus protecting the nonselective mineralocorticoid
receptor from occupation by glucocorticoids.
CC -1- CATALYTIC ACTIVITY: An 11-beta-hydroxysteroid + NAD(+) = an
11-oxosteroid + NADH.
CC -1- SUBUNIT: Interacts with ligand-free cytoplasmic NR3C2 (By
similarity).
CC -1- SUBCELLULAR LOCATION: Microsomal.
CC -1- TISSUE SPECIFICITY: Highly expressed in kidney, adrenal gland and
distal colon. Detected at much lower levels in lung.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
CC
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CC
CC ENBL; U2424; AAA87007.1; --
DR HSSP; P14061; 1FDU.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Microsome.
FT NP_BIND 82 111 NAD (BY SIMILARITY).
FT ACT_SITE 232 232 BY SIMILARITY.
SQ SEQUENCE 400 AA; 43726 MW; A1BAA328E2F189D CRC64;
Query Match 10.5%; Score 74.5; DB 1; Length 400;
Best Local Similarity 25.5%; Pred. No. 17;
Matches 38; Conservative 25; Mismatches 57; Indels 29; Gaps 6;
Qy 16 PTFGETDVMEALLRVKSE-----RLMLRALAGCGHVLPGTGASAIATVT 66
Db 7 PSGAWLLVAARALLQLRSLDRGPELLAALJALDWC-QLLPPPAALVVLGAG 65
Qy 67 PKGASMKLKPFR-POSTKSPSL-----RELRSKIREMKNKTSIQBSARVNRHLPGEHP 117
Db 66 WIALSRLARPPLPVATRAVLITCDTGFGKETAKKLDAMGFTVLATVLDLN-----GPG 120

QY 118 LLEKRAEYFRHLRSI-----KSGQVNRLL 141
Db 121 ALELRARCSPLKLLQMDLTPEDISRLV 149

RESULT 9

TLPB_BACSU STANDARD; PRT; 662 AA.
AC P39217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-accepting chemotaxis protein tlpB.
GN TLPB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / OI1085;
RX MEDLINE=94245722; PubMed=8186884;
RA Hanlon D.W., Ordal G.W.;
RT "Cloning and characterization of genes encoding methyl-accepting
chemotaxis proteins in Bacillus subtilis";
RL J. Biol. Chem. 269:14038-14046 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bron S.,
Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klexer-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapidine A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis";
RL Nature 390:249-256 (1997).
CC -1- FUNCTION: CHEMOTACTIC-SIGNAL TRANSDUCERS RESPOND TO CHANGES IN THE
CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT,
TRANSDUCE A SIGNAL FROM THE OUTSIDE TO THE INSIDE OF THE CELL, AND
FACILITATE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL
OF METHYLATION. ALL AMINO ACIDS SERVE AS ATTRACTANTS IN
B.SUBTILIS, THEY APPEAR TO CAUSE AN INCREASE IN THE TURNOVER
METHYL GROUPS, LEADING TO METHYLATION OF AN UNIDENTIFIED ACCEPTOR,
WHILE REPELLENTS HAVE BEEN SHOWN TO CAUSE A DECREASE IN METHYL
GROUP TURNOVER. THE METHYL GROUPS ARE ADDED BY A METHYLTRANSFERASE
AND REMOVED BY A METHYLESTERASE.
CC -1- SIMILARITY: Contains 1 methyl-accepting transducer domain.
CC -1- SIMILARITY: Contains 1 HAMP domain.

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DR EMBL; L29189; AAA20557.1; -;
DR EMBL; Z99119; CAB15101.1; -;
DR EMBL; Z99120; CAB15112.1; -;
DR PIR; D54078; D54078.
DR HSP; P02942; 1QU7.
DR Subtilisin; BG10862; tipB.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR004089; Chmtaxis_transd.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR003122; TarH.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR Pfam; PF02203; TarH; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
DR SMART; SM00319; TarH; 1.
DR PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
DR PROSITE; PS50885; HAMP; 1.
KW Chemotaxis; Transducer; Transmembrane; Methylation; Complete proteome.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 281
FT TRANSMEM 282 302
FT DOMAIN 303 662
FT DOMAIN 303 355
FT DOMAIN 374 610
FT MOD_RES 370 370
FT MOD_RES 594 594
FT MOD_RES 629 629
FT MOD_RES 636 636
SQ SEQUENCE 662 AA; 71535 MW; 91215F86293D7425 CRC64;

Query Match 10.5%; Score 74; DB 1; Length 662;
Best Local Similarity 24.1%; Pred. No. 35;
Matches 27; Conservative 26; Mismatches 53; Indels 6; Gaps 3;
QY 30 LEVKSERLAMLALAGMCHGVLPFGTASAIATVTP--KGASMKLPPRPQSTKSP- 86
DB 469 LETSKQDITSLNVINGIADQTNLLALNAIEARAGEYGRGFSVAEEVRLKAVQSADS 528
QY 87 LRELSRKIRENMKTIQBSA---RVNHLRPGHPLLEKRAEYFRHLRLSKSQ 135
DB 529 AKIEGLIQEIVREISTLSLMSFQSYNHEVKGGLQITDQTAESFKQIYEMTTQ 580

RESULT 10
VF2_BRD ID_VP2_BRD STANDARD; PRT; 908 AA.
AC P35934;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Structural core protein VP2.
GN S2.
OS Broadhaven virus (BRD).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10893;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93019012; PubMed=1328474;
RA Moss S.R., Jones L.D., Nuttall P.A.;
RT "Comparison of the major structural core proteins of tick-borne and
RT Culicoides-borne orbiviruses."

RL J. Gen. Virol. 73:2585-2590(1992).
CC -!- SIMILARITY: BELONGS TO THE REOVIRUSSES VP3 FAMILY.

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DR EMBL; M87875; -; NOT_ANNOTATED_CDS.
DR PIR; JQ1938; JQ1938.
DR HSP; P56582; 2BVV.
DR InterPro; IPR002614; Orbi_VP3.
DR Pfam; PF01700; Orbi_VP3; 1.
DR PDom; PD004438; Orbi_VP3; 1.
KW Core protein.
SQ SEQUENCE 908 AA; 102895 MW; 37A006EBD22CFEF7 CRC64;

Query Match 10.5%; Score 74; DB 1; Length 908;
Best Local Similarity 25.3%; Pred. No. 52;
Matches 22; Conservative 13; Mismatches 30; Indels 22; Gaps 2;
QY 73 KLKPPRPQSTKSP-ELSRKIRENMKTIQBSARVNHRLPE 114
DB 7 RVQTERQQNNSPYLRGDEVDHDPGIALSVFALQELIRKVRQSOTSLRNEGVEVNPAPPE 66
QY 115 GHPLLEKRAEYFRHLRLSKSQGVNRLI 141
DB 67 ----EQIFSAHLRLRDERPYRIETL 89

RESULT 11
VIOC_CHRVO ID_VIOC_CHRVO STANDARD; PRT; 429 AA.
AC Q9S3U9; Q9S0N3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT Probable monooxygenase vIOC (EC 1.-.-.-).
GN VIOC.
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=UCM51;
RX MEDLINE=20525185; PubMed=11075927;
RA August P.R., Grossman T.H., Minor C., Draper M.P., MacNeil I.A.,
RA Pemberton J.M., Call K.M., Holt D., Osburne M.S.;
RT "Sequence analysis and functional characterization of the violacein
RT biosynthetic pathway from Chromobacterium violaceum."
RL J. Mol. Microbiol. Biotechnol. 2:513-519(2000).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=JCM 1249;
RA Hoshino T.;
RT "Biosynthetic gene cluster for violacein pigment."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Prodeoxyviolacein + O(2) = deoxyviolacein.
CC -!- COFACTOR: FAD (Potential).
CC -!- PATHWAY: Violacein biosynthesis; common branch; second step.
CC -!- INDUCTION: By N-acylhomoserine lactone (AHL).
CC -!- BIOTECHNOLOGY: Violacein production is used as a biosensor for the
CC detection of quorum-sensing AHL production. Violacein possesses
CC antibacterial, antiviral, antimicrobial, antileishmanial,
CC trypanocidal and potential antitumoral activities.

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DR EMBL; AF172851; AAD51810.1; -;
DR EMBL; AB032799; BAA84784.1; -;
DR InterPro; IPR000733; Flav_monooxygenase.
DR Pfam; PF01360; Monooxygenase; 1.
KW Oxidoreductase; Monooxygenase; Flavoprotein; FAD;
FT NP_BIND 3 21 FAD (POTENTIAL).
FT CONFLICT 38 38 Q -> R (IN REF. 2).
FT CONFLICT 38 38 Q -> R (IN REF. 2).
SQ SEQUENCE 429 AA; 47948 MW; ALD1966CA9739895 CRC64;

Query Match 10.4%; Score 73.5; DB 1; Length 429;
Best Local Similarity 25.3%; Pred. No. 23;
Matches 41; Conservative 16; Mismatches 54; Indels 51; Gaps 8;

QY 3 STSTTNFAENRPTGCEFD-----VMREALLR-----VKSSERLAMLRA----- 43
DB 245 SPSLTTT-----DEPTWRAFDYFGGLPRDADEMLRQFLAKPSNDLINVRSSTHYKGN 300
QY 44 --LAGMCGHRVLPGTGASAIATVTPKGSMKMKPPR-----PQSTKSPSELREL 90
DB 301 VLLLGDAAHATAPFLG-----QGMMALEDARTVELLDRHQGDQKRAFFETTEL 350
QY 91 SRKIREMNKTIQESARVNHRLPEGHPLLEKRAEYFRHLRS 131
DB 351 ----RKVQADAMQDMARANYDVLSNPIFFWRARYTRYMHS 388

RESULT 12
ID_VGY3_HALSQ STANDARD; PRT; 437 AA.
AC P21561;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 50.6 kDa protein in the 5' region of gYrA and gYrB (ORF 3).
DE Haloferax sp. (strain Aa 2.2).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloferax.
OX NCBI_TaxID=2254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91100352; PubMed=1846146;
RA Holmes M.L., Dyall-Smith M.L.;
RT "Mutations in DNA gyrase result in novobiocin resistance in
RL J. Bacteriol. 173:642-648 (1991).
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DR EMBL; M38373; -; NOT ANNOTATED_CDS.
DR Hypothetical protein.
SQ SEQUENCE 437 AA; 50626 MW; B5B999A2AF3892BEF CRC64;

Query Match 10.4%; Score 73.5; DB 1; Length 437;
Best Local Similarity 29.5%; Pred. No. 24;
Matches 31; Conservative 9; Mismatches 44; Indels 21; Gaps 5;

QY 19 GETFDVREALLRVKSSERLAMLRLAGMCGHR-VLPGTGASAIATVTPKGSMKMK-- 75
DB 269 GEARGLPERPGLGVRTHVGGRLGRVGGAGRPQVPGDFA-----PQGEDSERRET 320

QY 76 PPRQSTKSPSELRLSKIREMNKTIQESARVNHRLPEGHPL 117
DB 321 PPRPHSRKRRTDGAHHRHRRRR-----RVHRREGALPAHP 358

RESULT 13
ID_PTNE_HUMAN STANDARD; PRT; 1187 AA.
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase pez).
GN PTEN14 OR PEZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95251727; PubMed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RA Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT ezrin-like domains";
RL Biochem. Biophys. Res. Commun. 209:959-965 (1995).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF HUMAN TISSUES
CC INCLUDING KIDNEY, SKELETAL MUSCLE, LUNG AND PLACENTA.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
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DR EMBL; X82676; CAA57993.1; -;
DR PIR; JC4155; JC4155.
DR HSP; P29350; 1GWZ.
DR Genew; HGNC:9647; PTFN14.
DR MIM; 603155;
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000387; TYR_Phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00373; Band 4.1; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND4.1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR Structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1121 1121 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
SQ SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;

Query Match 10.4%; Score 73.5; DB 1; Length 1187;
Best Local Similarity 27.3%; Pred. No. 79;
Matches 27; Conservative 19; Mismatches 16; Indels 37; Gaps 5;
QY 50 HRLVPG-TPGASIAATV-TPKASMKLK-----PPRPQ---STKSP 85
DB 521 NNVPSKPGASISHTVSTPLANKQLOSHNYSTAHMLKYLFRPPPPPRPPAISTP 580
QY 86 ELRE-----LSRKIRENMKTISQESARVNH 111
DB 581 DLASHRHRYVSGSPDLVTRKVLQSVKTFQBDSSPVVHQ 619
RESULT 14
VIF_HV1SC STANDARD; PRT; 109 AA.
AC P05899;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Viron infectivity factor (SOR protein) (Fragment).
GN VIF.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11702;
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC -!- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----
DR EMBL; M17450; AAA45059.1; -;
DR HIV; M17450; VIFSCC.
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PRO0349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
FT NON_TER
SQ SEQUENCE 109 AA; 12308 MW; 3D1B3599F78B727 CRC64;
Query Match 10.3%; Score 73; DB 1; Length 109;
Best Local Similarity 32.0%; Pred. No. 4.9;
Matches 32; Conservative 9; Mismatches 35; Indels 24; Gaps 6;
QY 22 FDMVEALLRVKSSERLAMLAL-AGWC-----GHRVLPPTGASIAATVTPKASMKLP 76
DB 29 FDCFS-----SAIRNAILGALVSGRCEYQAGHNKVGSLQYLALTALITFK-----KTRP 78
QY 77 PRPOSTKSPELRSRKIRENMKTISQESARVNHRLPEGH 116
DB 79 PLPSVRKLTEDR-----WNKPQKTGHRGSHTM-NGH 109
RESULT 15
FLID_VIBCH STANDARD; PRT; 666 AA.
AC Q9XQ63;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellar hook-associated protein 2 (HAP2) (Filament cap protein)
DE (Flagellar cap protein).
GN FLID OR VC2140.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
CC -!- FUNCTION: REQUIRED FOR THE MORPHOGENESIS AND FOR THE ELONGATION OF
CC THE FLAGELLAR FILAMENT BY FACILITATING POLYMERIZATION OF THE
CC FLAGELLIN MONOMERS AT THE TIP OF GROWING FILAMENT. FORMS A CAPPING
CC STRUCTURE, WHICH PREVENTS FLAGELLIN SUBUNIT (TRANSPORTED THROUGH
CC THE CENTRAL CHANNEL OF THE FLAGELLUM) FROM LEAKING OUT WITHOUT
CC POLYMERIZATION AT THE DISTAL END (BY SIMILARITY).
CC -!- SUBUNIT: Homopentamer (By similarity).
CC -!- SUBCELLULAR LOCATION: Flagellar.
CC -!- SIMILARITY: BELONGS TO THE FLID FAMILY.
CC -----
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CC -----
DR EMBL; A3004287; AAF95285.1; -;
DR PIR; G82111; G82111.
DR TIGR; VC2140; -;
DR InterPro; IPR003481; FLID.
DR Pfam; PF02465; FLID; 1.
KW Flagella; Coiled coil; Complete proteome.
FT DOMAIN 354 419 COILED COIL (POTENTIAL).
SQ SEQUENCE 666 AA; 72330 MW; 6794EFEC34A2A0D2 CRC64;
Query Match 10.3%; Score 73; DB 1; Length 666;
Best Local Similarity 25.4%; Pred. No. 44;
Matches 31; Conservative 21; Mismatches 52; Indels 18; Gaps 4;
QY 30 LRVKSSERLAMLALAGMCGHRVLPPTGASIAI-----AATVTPKASMKL-----K 75
DB 136 LDVQGNKSLVDI--VRGNGEKSNFGVRASINDVEGRLIVASVNGKDHVKMSAQAE 193
QY 76 PRPOSTKSPELRSRKIRENMKTISQESARVNHRLPEGHPLLEKRAEYFRHLRLSKSQ 135
DB 194 PGNP--LKQLEYKTLQVRVRLDKARAQAQLIAPLTPEQKVAAKVAEKIGDAARLVQD 251
QY 136 GV 137
DB 252 EV 253
RESULT 16
PHSA_STRAT STANDARD; PRT; 642 AA.
ID PHSA_STRAT
AC Q53692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

345 RPVPVDFDITLPLVLSAA-----PAERFDLLVDPRALGGRLRLVDKPGGAPACTPDPLG- 398

Db 345 RPVPVDFDITLPLVLSAA-----PAERFDLLVDPRALGGRLRLVDKPGGAPACTPDPLG- 398

Qy 71 SMKLKPPRPOSTKSPDLRLSKIRZ-----MKNKTISOESARVNHRLPEGHPLL 119

Db 399 -----GVRYPEYMEF--RVRETCEBSPALPEVLGSPFRMSHDIPGHRLI 443

NCBI_TaxID=1890;

SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.

STRAIN=IMRU 3720;

MEDLINE=96011355; PubMed=7592317;

Hsieh C.-J., Jones G.H.;

"Nucleotide sequence, transcriptional analysis, and glucose regulation of the phenoxazinone synthase gene (phaA) from Streptomyces antibioticus.";

J. Bacteriol. 177:5740-5747(1995).

[2]

SUBUNITS.

MEDLINE=82066838; PubMed=73053984;

Choy H.A.; Jones G.H.;

"Phenoxazinone synthase from Streptomyces antibioticus: purification of the large and small enzyme forms.";

Arch. Biochem. Biophys. 211:55-65(1981).

CC -!- FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.

CC -!- CATALYTIC ACTIVITY: 4,4-methyl-3-hydroxyanthraniloyl pentapeptide + 3 O(2) = 2 actinomycin acid + 6 H(2)O.

CC -!- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHETEROMER (LARGE FORM).

CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -!- SIMILARITY: Contains 2 plastocyanin-like domains.

CC

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CC

EMBL; U04283; AAA86668.1; ALT_INIT.

HSP; F36649; 1K7.

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR002355; MultiCu oxidase2.

DR Pfam; PF00394; Cu-oxidase; 1.

DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

KW Oxidoreductase; Repeat; Metal-binding; Copper;

KW Antibiotic biosynthesis.

INIT_MET 0

DOMAIN 86 223

FT DOMAIN 86 223 PLASTOCYANIN-LIKE 1.

FT DOMAIN 493 620 PLASTOCYANIN-LIKE 2.

FT METAL 161 161 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 163 163 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 201 201 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 203 203 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 524 524 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 527 527 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 529 529 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 602 602 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 603 603 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 604 604 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 608 608 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 613 613 COPPER (TYPE 1) (BY SIMILARITY).

SQ SEQUENCE 642 AA; 70113 MW; E0B39C0BA3364E48 CRC64;

Query Match 10.2%; Score 72; DB 1; Length 642;

Best Local Similarity 25.6%; Pred. No. 52;

Matches 30; Conservative 17; Mismatches 40; Indels 30; Gaps 6;

15 RPT---FGETEDVMEALLRVKSSERLAMLALAGMCGHRY-LFGTGASAIATVTPKGA 70

Qy

Phenoxazinone synthase (EC 1.-.-.-) (PHS).

PHSA.

Streptomyces antibioticus.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Streptomyces; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1890;

SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.

STRAIN=IMRU 3720;

MEDLINE=96011355; PubMed=7592317;

Hsieh C.-J., Jones G.H.;

"Nucleotide sequence, transcriptional analysis, and glucose regulation of the phenoxazinone synthase gene (phaA) from Streptomyces antibioticus.";

J. Bacteriol. 177:5740-5747(1995).

[2]

SUBUNITS.

MEDLINE=82066838; PubMed=73053984;

Choy H.A.; Jones G.H.;

"Phenoxazinone synthase from Streptomyces antibioticus: purification of the large and small enzyme forms.";

Arch. Biochem. Biophys. 211:55-65(1981).

CC -!- FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.

CC -!- CATALYTIC ACTIVITY: 4,4-methyl-3-hydroxyanthraniloyl pentapeptide + 3 O(2) = 2 actinomycin acid + 6 H(2)O.

CC -!- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHETEROMER (LARGE FORM).

CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -!- SIMILARITY: Contains 2 plastocyanin-like domains.

CC

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CC

EMBL; U04283; AAA86668.1; ALT_INIT.

HSP; F36649; 1K7.

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR002355; MultiCu oxidase2.

DR Pfam; PF00394; Cu-oxidase; 1.

DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

KW Oxidoreductase; Repeat; Metal-binding; Copper;

KW Antibiotic biosynthesis.

INIT_MET 0

DOMAIN 86 223

FT DOMAIN 86 223 PLASTOCYANIN-LIKE 1.

FT DOMAIN 493 620 PLASTOCYANIN-LIKE 2.

FT METAL 161 161 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 163 163 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 201 201 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 203 203 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 524 524 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 527 527 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 529 529 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 602 602 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 603 603 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 604 604 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 608 608 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 613 613 COPPER (TYPE 1) (BY SIMILARITY).

SQ SEQUENCE 642 AA; 70113 MW; E0B39C0BA3364E48 CRC64;

Query Match 10.2%; Score 72; DB 1; Length 642;

Best Local Similarity 25.6%; Pred. No. 52;

Matches 30; Conservative 17; Mismatches 40; Indels 30; Gaps 6;

15 RPT---FGETEDVMEALLRVKSSERLAMLALAGMCGHRY-LFGTGASAIATVTPKGA 70

Qy

Phenoxazinone synthase (EC 1.-.-.-) (PHS).

PHSA.

Streptomyces antibioticus.

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Streptomyces; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1890;

SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.

STRAIN=IMRU 3720;

MEDLINE=96011355; PubMed=7592317;

Hsieh C.-J., Jones G.H.;

"Nucleotide sequence, transcriptional analysis, and glucose regulation of the phenoxazinone synthase gene (phaA) from Streptomyces antibioticus.";

J. Bacteriol. 177:5740-5747(1995).

[2]

SUBUNITS.

MEDLINE=82066838; PubMed=73053984;

Choy H.A.; Jones G.H.;

"Phenoxazinone synthase from Streptomyces antibioticus: purification of the large and small enzyme forms.";

Arch. Biochem. Biophys. 211:55-65(1981).

CC -!- FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.

CC -!- CATALYTIC ACTIVITY: 4,4-methyl-3-hydroxyanthraniloyl pentapeptide + 3 O(2) = 2 actinomycin acid + 6 H(2)O.

CC -!- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHETEROMER (LARGE FORM).

CC -!- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -!- SIMILARITY: Contains 2 plastocyanin-like domains.

CC

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CC

EMBL; U04283; AAA86668.1; ALT_INIT.

HSP; F36649; 1K7.

InterPro; IPR001117; Cu-oxidase.

InterPro; IPR002355; MultiCu oxidase2.

DR Pfam; PF00394; Cu-oxidase; 1.

DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

KW Oxidoreductase; Repeat; Metal-binding; Copper;

KW Antibiotic biosynthesis.

INIT_MET 0

DOMAIN 86 223

FT DOMAIN 86 223 PLASTOCYANIN-LIKE 1.

FT DOMAIN 493 620 PLASTOCYANIN-LIKE 2.

FT METAL 161 161 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 163 163 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 201 201 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 203 203 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 524 524 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 527 527 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 529 529 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 602 602 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 603 603 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 604 604 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 608 608 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 613 613 COPPER (TYPE 1) (BY SIMILARITY).

SQ SEQUENCE 642 AA; 70113 MW; E0B39C0BA3364E48 CRC64;

Query Match 10.2%; Score 72; DB 1; Length 642;

Best Local Similarity 25.6%; Pred. No. 52;

Matches 30; Conservative 17; Mismatches 40; Indels 30; Gaps 6;

15 RPT---FGETEDVMEALLRVKSSERLAMLALAGMCGHRY-LFGTGASAIATVTPKGA 70

Qy

FT METAL 113 113 SUBUNIT.
FT METAL 116 116 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 119 119 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 123 123 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 152 152 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 155 155 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 158 158 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 162 162 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 212 AA; 23896 MW; 4D5F95E4C918FE8 CRC64;
Query Match 10.1%; Score 71.5; DB 1; Length 212;
Best Local Similarity 30.9%; Pred. No. 15;
Matches 29; Conservative 19; Mismatches 35; Indels 11; Gaps 5;
QY 39 AMLRALMGCHRVLPVGTGASAIAT--VTPKGASMKLPPRQSTKSPKPELRELSKIR 95
DB 12 ALAQQAARAGHASVRLGHSSAVATKYVNLRFPSMDKSVTDRAQTLLWTEL---IR 68
QY 96 ENKTKTIS---QESARVNRHRLPEGHPLLEK-RAEY 125
DB 69 GLGMTLSVLFREPATINYPFEKG-PLSPRFRGEH 101
RESULT 20
PGK_NEIMA
ID PGK_NEIMA STANDARD; PRT; 392 AA.
AC Q9JWS8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR NMA0257.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10763919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagsels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
RL Nature 404:502-506(2000).
CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate.
CC -!- PATHWAY: Second phase of glycolysis; second step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
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CC EMBL; AL162752; CAB033565.1; --
DR PIR; E82020; E82020.
DR HSSP; P18912; 1PHP.
DR HAWAP; MF_00145; 1.
DR InterPro; IPR001576; PGK.
DR Pfam; PF0162; PGK; 1.
DR PRINTS; PR00477; PGKLYCKINASE.
DR PROSITE; PS00111; PGKLYCERATE_KINASE; 1.

KW Transferase; Kinase; Glycolysis; Complete proteome.
SQ SEQUENCE 392 AA; 40661 MW; F6AB86C6C7BFED35 CRC64;
Query Match 10.1%; Score 71.5; DB 1; Length 392;
Best Local Similarity 25.0%; Pred. No. 32;
Matches 37; Conservative 17; Mismatches 53; Indels 41; Gaps 7;
QY 13 ENRPTGETFDVNRALLRVKSSER---LAMLRALAGMC-----CHRVLPVGTGAS 59
DB 97 ENKPAL-NAGDVVMLQNVAINKEKNDLELKGAYASLDCVFNDAFGTAHRAQASTEAV 155
QY 60 AIAATVTPKGASKM-----LKPPRPQ-----STKSPPELRELSKIREM--- 97
DB 156 AQAAPVACAGVLMAEGLDALKALQKAPRPMVAIVAGSKVSTKLITLESADKVDQLIVG 215
QY 98 ---NKTISOESARVNRHRLPEGHPLLEK 121
DB 216 GGANTFLLAEGKAIGKSLAE-HDLVEE 242
RESULT 21
PGK_NEIMB
ID PGK_NEIMB STANDARD; PRT; 392 AA.
AC Q9K1R0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR NMB0010.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clechko A., Parksey D.S., Blair E., Ciftone H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
RL Science 287:1809-1815(2000).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Bairoch A.;
RL Unpublished observations (OCT-2002).
CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate.
CC -!- PATHWAY: Second phase of glycolysis; second step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC -!- CAUTION: This is a conceptual translation: a probable incorrect perfect sequence repeat was excised.
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CC EMBL; AE002359; AAF40489.1; --
DR PIR; H81247; H81247.
DR HSSP; P18912; 1PHP.
DR TIGR; NMB0010; --

[illegible]

Simoni P., Kempf J.;
"Human choline acetyltransferase (CHAT): partial gene sequence and
potential control regions."; Genomics 12:412-416(1992).
[5]
SEQUENCE OF 688-738 FROM N.A.
TISSUE=Lymphocytes;
MEDLINE=92149876; PubMed=1784419;
Cervini R., Rocchi M., Didonato S., Finocchiaro G.;
"Isolation and sub-chromosomal localization of a DNA fragment of the
human choline acetyltransferase gene."; Neurosci. Lett. 132:191-194(1991).
-!- FUNCTION: Catalyzes the reversible synthesis of acetylcholine
(ACh) from acetyl CoA and choline at cholinergic synapses.
-!- CATALYTIC ACTIVITY: Acetyl-CoA + choline = CoA + O-acetylcholine.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
NamesM; Synonyms=83 kDa;
IsoId=P28329-1; Sequence=Displayed;
NamesS; Synonyms=74 kDa;
IsoId=P28329-2; Sequence=VSP_000790;
NamesR; Synonyms=70 kDa;
IsoId=P28329-3; Sequence=VSP_000791;
-!- DISEASE: Defects in CHAT are the cause of familial infantile
myasthenia gravis 2 (FMG2) [MIM:254210]; also known as CMS-EA.
FMG2 patients have myasthenic symptoms since birth or early
infancy, negative tests for anti-AChR antibodies, and abrupt
episodic crises with increased weakness, bulbar paralysis, and
apnea precipitated by undue exertion, fever, or excitement.
Inheritance is autosomal recessive.
-!- SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
FAMILY.
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or send an email to license@isb-sib.ch).

EMBL; S56138; AAA14245.1; -
EMBL; AF305907; AAK08953.1; -
EMBL; AF305906; AAK08950.1; -
EMBL; AF305894; AAK08950.1; JOINED.
EMBL; AF305895; AAK08950.1; JOINED.
EMBL; AF305896; AAK08950.1; JOINED.
EMBL; AF305897; AAK08950.1; JOINED.
EMBL; AF305898; AAK08950.1; JOINED.
EMBL; AF305899; AAK08950.1; JOINED.
EMBL; AF305900; AAK08950.1; JOINED.
EMBL; AF305901; AAK08950.1; JOINED.
EMBL; AF305902; AAK08950.1; JOINED.
EMBL; AF305903; AAK08950.1; JOINED.
EMBL; AF305904; AAK08950.1; JOINED.
EMBL; AF305905; AAK08950.1; JOINED.
EMBL; AF305908; AAK08954.1; -
EMBL; AF305906; AAK08951.1; -
EMBL; AF305894; AAK08951.1; JOINED.
EMBL; AF305895; AAK08951.1; JOINED.
EMBL; AF305896; AAK08951.1; JOINED.
EMBL; AF305897; AAK08951.1; JOINED.
EMBL; AF305898; AAK08951.1; JOINED.
EMBL; AF305899; AAK08951.1; JOINED.
EMBL; AF305900; AAK08951.1; JOINED.
EMBL; AF305901; AAK08951.1; JOINED.
EMBL; AF305902; AAK08951.1; JOINED.
EMBL; AF305903; AAK08951.1; JOINED.
EMBL; AF305904; AAK08951.1; JOINED.
EMBL; AF305905; AAK08951.1; JOINED.
EMBL; AF305909; AAK08955.1; -
EMBL; AF305906; AAK08952.1; -
EMBL; AF305894; AAK08952.1; JOINED.

```

FT CONFLICT 604 608 MISSING (IN REF. 2).
FT CONFLICT 714 714 L -> S (IN REF. 2).
FT CONFLICT 1189 1189 E -> K (IN REF. 2).
FT CONFLICT 1193 1193 E -> K (IN REF. 2).
FT CONFLICT 1331 1331 G -> S (IN REF. 1).
SQ SEQUENCE 2564 AA; 289982 MW; 52CDE7D11D601ECC CRC64;

Query Match 10.1%; Score 71.5; DB 1; Length 2564;
Best Local Similarity 24.5%; Pred. No. 3e+02;
Matches 34; Conservative 17; Mismatches 71; Indels 17; Gaps 5;

QY 12 AENRPTFGETFDVREALLRVKSSERLAMLALAGMCGHRVLPGTGASAIATVTPKGAS 71
DB 2170 AEVTRVVG-----YVQEQEKPELQPRDRLEPEIPGRVEPAALPAEPDAAETPATP--AA 2223
QY 72 MKLKPPRPQSTKSP-ELELSRKIR-EMNKTISQESARVNHRLPE-----GHPLLE 120
DB 2224 ABQVPRPRPQESADRAEELPRRRPRPQESVDQSEEAARRRPERQESAHEAAHSLT 2283
QY 121 KEAEVFRHLRSLKSGQVNR 139
DB 2284 GYEQWERRRRERLER 2302

RESULT 26
VIF HVIRH STANDARD; PRT; 192 AA.
ID VIF HVIRH AC P05500;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI TaxID=11701;
RN [1]_TaxID=11701;
RP SEQUENCE FROM N.A.
RA Starcich B.R., Hann B.H., Shaw G.M., McNeely P.D., Modrow S.,
RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
RA Wong-Skaal F.;
RL Submitted (XXX-1987) to the HIV data bank.
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; M17451; AAA45054.1;
CC HIV; M17451; VIFSRF.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; P00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFCT.
CC DR PRODOM; PD000063; Viral_infect; 1.
CC AIDS.
SQ SEQUENCE 192 AA; 22687 MW; F005E0AE621A5C6C CRC64;

Query Match 10.0%; Score 71; DB 1; Length 192;
Best Local Similarity 29.5%; Pred. No. 15;
Matches 28; Conservative 9; Mismatches 44; Indels 14; Gaps 4;

QY 22 FDMVREALLRVKSSERLAMLALAGMCGHRVLPGTGASAIATVTPKGASMKLKPPRPOS 81
DB 112 FDCPSAIRKPSLGHIVSPRC-EYQAGHNKVGSLQYLALALTTPK-----KIKPLPSV 166
QY 82 TKSPLELSRKIRVNMKTISQESARVNHRLPEGH 116
DB 167 KULTDR-----WNKPKTKGHRGSHTM-NGH 192

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RESULT 27
HIT_PIG
ID HIT_PIG STANDARD; PRT; 211 AA.
AC P06348;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histone H1t.
GN H1t.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=85054795; PubMed=6389534;
RA Cole K.D., York R.G., Kistler W.S.;
RT "The amino acid sequence of boar H1t, a testis-specific H1 histone
variant.";
RL J. Biol. Chem. 259:13695-13702(1984).
CC -!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: THIS HISTONE IS A TESTIS-SPECIFIC H1 VARIANT
CC THAT APPEARS DURING MEIOSIS IN SPERMATOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
DR PIR; A02581; HSPG1T.
DR HSSP; P08287; 1GHC.
DR InterPro; IPR005818; Histone_H1/H5.
DR InterPro; IPR005819; Histone_H5.
DR Pfam; PF00538; linker_Histone; 1.
DR PRINTS; PR00624; HISTONEH5.
DR SMART; SM00526; H15; 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
KW Acetylation; Spermatogenesis; Testis.
FT MOD_RES 1 ACETYLATION.
FT DOMAIN 39 112 GLOBULAR.
SQ SEQUENCE 211 AA; 22059 MW; EAC47C51A8F5364 CRC64;
Query Match 10.0%; Score 71; DB 1; Length 211;
Best Local Similarity 21.3%; Pred. No. 17;
Matches 27; Conservative 29; Mismatches 49; Indels 22; Gaps 5;
QY 8 TNFAENPTGTFDYNREALLRV-----KSSERLAMLRLAGMCHRVL---PGTGAS 59
DB 48 TEALSVSOERAGMSLAALKALAAAGYDVKNNGRIKL--GLKSLVGKILVQTRGTGAS 105
QY 60 A---IAATVTPKGSMKLPKPPRPOST-----KSPLELSELRKIRENMKNTISQESAR 107
DB 106 GSFKLKKAPEPRKGVKPKAAAKTKLVLSRDSKSPKSAKANKRAKRSRTTAAQKAAR 165
QY 108 VNHRLPE 114
DB 166 SGRKTK 172
RESULT 28
HSF7_ARATH
ID_HSF7_ARATH STANDARD; PRT; 377 AA.
AC Q9TCD3; Q9SCW3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heat shock factor protein 7 (HSF 7) (Heat shock transcription factor
7) (HSF 7).
GN HSF7 OR AT4G11660 OR TSC23.90
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
RA Mayer K.P.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Dueterhoeft A., Stiekema W., Ertan K.-D., Terry N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hehseisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weijens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
RA Moolijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
RA Pettitt A., Raebdrem M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Blocher H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarsee A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chénor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dredia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Stonking T., Kalicki J., Sheet P., Cordes M., Abu-Threideh J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Grnat S., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana.";
RL Nature 402:769-777(1999).
RN [2]
RP SEQUENCE OF 50-377 FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Green siliques;
RA Schoeffl F., Praendl R.;
RT "De-repression of heat shock protein synthesis in transgenic plants.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
CC PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
CC SIMILARITY).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- PTM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HSF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL049500; CAB39937.1; -.

DR EMBL: AL161532; CAB78209.1; --
 DR EMBL: AJ251868; CAB63803.1; --
 DR PIR: T04213; T04213.
 DR HSSP: P22813; 1HKT.
 DR InterPro: IPR000232; HSF_DNA_bind.
 DR InterPro: IPR002341; HSF_ETS.
 DR Pfam: PF00447; HSF_DNA_bind; 1.
 DR PRINTS: PR00056; HSFDOMAIN.
 DR ProDom: PD001788; HSF_DNA_bind; 1.
 DR SMART: SM00415; HSF; 1.
 DR PROSITE: PS00434; HSF_DOMAIN; 1.
 KW Transcription regulation; Nuclear protein; DNA-binding; Activator;
 KW Phosphorylation; Heat shock; Multigene family.
 FT DNA_BIND 57 151 BY SIMILARITY.
 FT DOMAIN 14 21 POLY-GLY.
 FT DOMAIN 32 50 POLY-GLY.
 FT DOMAIN 155 171 POLY-ALA.
 FT DOMAIN 202 207 POLY-ALA.
 FT CONFLICT 50 50 G -> R (IN REF. 2).
 FT SEQUENCE 377 AA; 39705 MW; FDI5ES95B7FCS84 CRC64;
 Query Match 10.0%; Score 71; DB 1; Length 377;
 Best Local Similarity 28.4%; Pred. No. 34;
 Matches 27; Conservative 14; Mismatches 24; Indels 30; Gaps 5;
 QY 54 PGTGASAIATVTPKGASMKLPPRQSTKSPFLSKIRKRENMKTKISQESARVN--- 109
 Db 201 PAAAAAAGGVW---GGSLQ-----RTTCTTAPLVEENLRKONERLRKEMTKLGLY 254
 QY 110 -----HRLPEGHP--LLEKRAE 124
 Db 255 ANIYTLMANFTPQEDCAHLLPEGKPLDLLPERQE 289
 RESULT 29
 APMG_PYRAB STANDARD; PRT; 410 AA.
 ID APMG_PYRAB
 AC Q9V2N6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
 DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (aPGAM).
 GN APMG OR PYRAB00490 OR PAR2318.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GS5 / Orsay;
 RX PubMed=12622808;
 RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
 RA Pech O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
 RT "An integrated analysis of the genome of the hyperthermophilic
 archaeon Pyrococcus abyssi.";
 RL Mol. Microbiol. 47:1495-1512(2003).
 CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
 CC 3-phosphoglycerate (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
 CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
 CC FAMILY. A-PGAM SUBFAMILY.
 CC
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 CC
 CC EMBL: AJ248283; CAB48972.1; --

DR PIR: E75190; E75190.
 DR HAMAP: MF_01402; --; 1.
 DR InterPro: IPR004456; BcpB.
 DR InterPro: IPR006124; Metalloenzyme.
 DR Pfam: PF01676; Metalloenzyme; 1.
 DR ProDom: PD004704; BcpB; 1.
 DR TIGRFAMs: TIGR003106; bcpB; 1.
 KW Isomerase; Complete proteome.
 SQ SEQUENCE 410 AA; 45201 MW; 91C8A89637608826 CRC64;
 Query Match 10.0%; Score 71; DB 1; Length 410;
 Best Local Similarity 22.7%; Pred. No. 37;
 Matches 29; Conservative 21; Mismatches 52; Indels 26; Gaps 4;
 QY 13 ENRRFTFGTDFVMEALL-----RVKSSRLAMLRAL-----AGMCGHRVLP 54
 Db 91 EDDLAFRVNFATLKGIVDRAGRISTEAEHAELAKAIQEVGVDFIFKATGCHRAVL 150
 QY 55 GTGASAIATVTPKGASMKLPPRQSTKSPFLSKIRKRENMKTKISQESARVNHRLE 114
 Db 151 VLKGMADGYRVGDNDPHVEGKPPHKSWEDEE-----SKKVAE-----ILEEPVKKAEVLE 202
 QY 115 GHPLEKR 122
 Db 203 RHPINEKR 210
 RESULT 30
 APMG_PYRFU STANDARD; PRT; 411 AA.
 ID APMG_PYRFU
 AC P58814;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
 DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (aPGAM).
 GN APMG OR PF1959.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RX MEDLINE=22071963; PubMed=12076795;
 RA van der Oost J., Huynen M.A., Vernees C.H.;
 RT "Molecular characterization of phosphoglycerate mutase in archaea.";
 RL FEMS Microbiol. Lett. 212:111-120(2002).
 CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
 CC 3-phosphoglycerate.
 CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
 CC -!- COFACTOR: Magnesium (Probable).
 CC -!- ENZYME REGULATION: Inhibited to approximately 20% by EDTA.
 CC -!- SUBUNIT: Homotetramer (Probable).
 CC -!- MISCELLANEOUS: Optimal pH is 8.0.
 CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
 CC FAMILY. A-PGAM SUBFAMILY.
 CC
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 CC
 CC EMBL: AE010289; AAL82083.1; --

DR HAMAP; MF_01402; -; 1.
 DR InterPro; IPR004456; BcbP.
 DR InterPro; IPR006124; Metalloenzyme.
 DR Pfam; PF01676; Metalloenzyme; 1.
 DR ProDom; PD004704; BcbP; 1.
 DR TIGRFAMs; TIGR00306; bcbP; 1.
 KW Isomerase; Magnesium; Complete proteome.
 SQ SEQUENCE 411 AA; 45314 MW; 870587E630C2B104 CRC64;
 Query Match 10.0%; Score 71; Length 411;
 Best Local Similarity 26.2%; Pred. No. 37;
 Matches 28; Conservative 14; Mismatches 39; Indels 26; Gaps 5;
 QY 31 RVKSERLAMLRL-----AGMCHR---VLPCTGASAIATVTPKGASKLX 75
 Db 116 RISTEEAHELAKAQNVDVIFGATGRHVLVKGVAEGYKGVNDPHEAG---K 172
 QY 76 PPRFQSTKSPELRSLKIREMNTKTIQESARVNHRLPEGHPLLEKR 122
 Db 173 FPHFPTWED----EASKKVAE-----ILEEFVKAHEVLDRHPINEXR 211
 RESULT 31
 RNE_ECOLI
 ID - RNE_ECOLI STANDARD; PRT; 1061 AA.
 AC P21513; P77591;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease E (EC 3.1.4.-) (RNase E).
 GN RNE OR AMS OR HMP1 OR B1084.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampaio G., Seki Y., Tagami H., Takemoto K., Wada C., Yanamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 RN [3]
 RP SEQUENCE OF 1-1025 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=93078265; PubMed=1447789;
 RA Casaregola S., Jacq A., Laoudj D., McGurk G., Margaron S.,
 RA Tempete M., Norris V., Holland I.B.;
 RT "Cloning and analysis of the entire Escherichia coli ams gene. ams is
 RT identical to hmp1 and encodes a 114 kDa protein that migrates as a
 RT 180 kDa protein.";
 RL J. Mol. Biol. 228:30-40(1992).
 RN [4]
 RP SEQUENCE OF 1-844 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91131576; PubMed=1704367;
 RA Claverie-Martin F., Diaz-Torres M., Yancey S.D., Kushner S.R.;

RT "Analysis of the altered mRNA stability (ams) gene from Escherichia
 RT coli. Nucleotide sequence, transcriptional analysis, and homology of
 RT its product to MRP3, a mitochondrial ribosomal protein from
 RT Neurospora crassa.";
 RL J. Biol. Chem. 266:2843-2851(1991).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
 RC STRAIN=K12;
 RX MEDLINE=91187608; PubMed=2011493;
 RA Chauhan A.K., Miczak A., Taraseviciene L., Apirion D.;
 RT "Sequencing and expression of the rne gene of Escherichia coli.";
 RL Nucleic Acids Res. 19:125-129(1991).
 RN [6]
 RP SEQUENCE OF 844-1061 FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=K12;
 RX MEDLINE=94022304; PubMed=8415644;
 RA Cormack R.S., Genereux J.L., Mackie G.A.;
 RT "RNase E activity is conferred by a single polypeptide:
 RT overexpression, purification, and properties of the ams/rne/hmp1 gene
 RT product.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:9006-9010(1993).
 RN [7]
 RP CHARACTERIZATION.
 RX PubMed=11328869;
 RA Walsh A.P., Tock M.R., Mallen M.H., Kabardin V.R., Gabain Av A.,
 RA McDowall K.J.;
 RT "Cleavage of poly(A) tails on the 3'-end of RNA by ribonuclease E of
 RT Escherichia coli.";
 RL Nucleic Acids Res. 29:1864-1871(2001).
 CC -1- FUNCTION: NATURES 5S RNA FROM ITS PRECURSORS FROM ALL THE RNA
 CC GENES. IT ALSO CLEAVES RNA I, A MOLECULE THAT CONTROLS THE
 CC REPLICATION OF COLE1 PLASMID DNA. IT IS THE MAJOR ENDO-RIBONUCLEASE
 CC PARTICIPATING IN MRNA TURNOVER IN E.COLI. IT INITIATES THE DECAY
 CC OF RNAs BY CUTTING THEM INTERNALLY NEAR THEIR 5'-END. IT IS ABLE
 CC TO REMOVE POLY(A) TAILS BY AN ENDO-NUCLEOLYTIC PROCESS.
 CC -1- SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESSOME OR RNA
 CC DEGRADOSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE RNE FAMILY.
 CC -1- SIMILARITY: Contains 1 SI motif domain.
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1003
 CC ONWARD AND IS SHORTER (1025 AA) DUE TO A FRAMESHIFT.
 CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS
 CC AND IS SHORTER (815 AA) DUE TO A FRAMESHIFT.
 CC -1- CAUTION: REF.5 SEQUENCE WAS ALSO INCORRECT IN MANY POSITIONS DUE
 CC TO FRAMESHIFTS.
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 CC -----
 DR EMBL; A5000209; AAC74168.1; -;
 DR EMBL; D90744; BAA35893.1; -;
 DR EMBL; X67470; CAA47818.1; ALT_FRAME.
 DR EMBL; M62747; AAA23443.1; ALT_FRAME.
 DR EMBL; X54309; AAA38206.1; ALT_FRAME.
 DR EMBL; L23942; AAA03347.1; -;
 DR PIR; A64852; S27311.
 DR ECoGene; EGI0859; rne.
 DR InterPro; IPR004659; RNaseEG.
 DR InterPro; IPR003029; S1.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR TIGRFAMs; TIGR00757; RNaseEG; 1.
 DR PROSITE; P850126; S1; 1.
 DR Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.
 KW DOMAIN 39 119 SI MOTIF.
 FT STRAIN=K12;
 RX MEDLINE=91131576; PubMed=1704367;
 RA Claverie-Martin F., Diaz-Torres M., Yancey S.D., Kushner S.R.;
 FT CONFLICT 390 390 Q -> H (IN REF. 4).
 FT CONFLICT 487 487 V -> L (IN REF. 1 AND 2).
 FT

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DR PROSITE; PS00661; FERM_2; 1.
DR DR PROSITE; PS0057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
DR KW structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM
FT .DOMAIN 935 1189 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1123 1223 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 635 639 POLY-GLY.
FT DOMAIN 712 718 POLY-GLU.
FT SEQUENCE 1189 AA; 135030 MW; 2B85BE5F9C723303 CRC64;

Query Match          10.0%; Score 71; DB 1; Length 1189;
Best Local Similarity 26.0%; Pred. No. 1.3e+02;
Matches 26; Conservative 19; Mismatches 17; Indels 38; Gaps 5;

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[illegible]

FT DOMAIN 1285 1289 POLY-LYS.
FT DOMAIN 1375 1386 POLY-LYS.
FT DOMAIN 1398 1405 POLY-LYS.
FT VARIANT 53 53 W -> R (in TCS).
FT VARIANT 439 439 /FTID=VAR_005630.
FT VARIANT 810 810 P -> L.
FT VARIANT 1313 1313 /FTID=VAR_005631.
FT VARIANT 1355 1355 A -> V.
FT VARIANT 1313 1313 /FTID=VAR_005632.
FT VARIANT 1355 1355 A -> V (in dbSNP:15251).
FT VARIANT 1313 1313 /FTID=VAR_005633.
FT VARIANT 1355 1355 D -> G.
FT VARIANT 1312 1312 /FTID=VAR_005634.
FT VARIANT 1411 1411 K -> Q (IN REF. 2).
FT CONFLICT 1411 1411 MW; 144312 MW; 38804030985C2699 CRC64;
SQ SEQUENCE 1411 AA; 144312 MW; 38804030985C2699 CRC64;

Query Match 10.0%; Score 70.5; DB 1; Length 1411;
Best Local Similarity 21.2%; Pred. No. 1.8e+02;
Matches 31; Conservative 19; Mismatches 47; Indels 49; Gaps 5;

QY 5 STTTNVAENR-----PTGG-----ETFDVMEALLRVKSSERLAML 41
DB 164 SANTTLVSETEEGSVPAFGAAAKPMWAGAGADSSSEDTSSTSDTDEVEKASEKILQV 223
QY 42 RALAGMCHRVLPFGTGASAIATVTPKG----ASMKLKPPRPQSTKSPPELRELSRKIREM 97
DB 224 RAASA-----PAKGTGPKGATPAPPKAGAVASQTKAGKPE-----ED 261
QY 98 NKTISCSARVNHRLPEGHPLLEKRA 123
DB 262 SSSSESSSEETPAKALLOAKA 287

RESULT 35
PHNJ_ECOLI STANDARD; PRT; 281 AA.
AC F16688; 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE PHNJ protein.
GN PHNJ OR B4098.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91193228; PubMed=1840580;
RA Makino K., Kim S.K., Shinagawa H., Amemura M., Nakata A.;
RT "Molecular analysis of the cryptic and functional phn operons for
phosphate use in Escherichia coli K-12.";
RL J. Bacteriol. 173:2665-2672(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B.
RX MEDLINE=90170953; PubMed=2155230;
RA Chen C.-M., Ye Q.-Z., Zhu Z., Wanner B.L., Walsh C.T.;
RT "Molecular biology of carbon-phosphorus bond cleavage. Cloning and
sequencing of the phn (psid) genes involved in alkylphosphonate
uptake and C-P lyase activity in Escherichia coli B.";
RL J. Biol. Chem. 265:4461-4471(1990).
CC -!- FUNCTION: BELONGS TO AN OPERON INVOLVED IN ALKYLPHOSPHONATE

CC UPTAKE AND C-P LYASE. EXACT FUNCTION NOT KNOWN.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN K12.
CC -!- SIMILARITY: BELONGS TO THE PHNJ FAMILY.
CC -----
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CC -----
CC EMBL; D90227; BAA14270.1; -
CC EMBL; U14003; AAM96997.1; -
CC EMBL; AE000482; AAC77059.1; -
CC EMBL; J05260; AAA24348.1; -
CC PIR; A65219; A65219.
CC EcoGene; EG10719; phnJ.
KW Alkylphosphonate uptake; Complete proteome.
FT VARIANT 103 103 V -> L (IN STRAIN B)
SQ SEQUENCE 281 AA; 31845 MW; 241F6AF140995468 CRC64;

Query Match 9.9%; Score 70; DB 1; Length 281;
Best Local Similarity 23.8%; Pred. No. 29;
Matches 36; Conservative 27; Mismatches 52; Indels 36; Gaps 8;

QY 19 GETFDVMEALLRVKSSERLAMLALAGMCHRV-----LP---GTGASAIATVTP 67
DB 6 GYNFAYLDE---QTKRMIRAILKAVA-IPGYQVFGREMPYMGWGTGIGLTASVIG 61
QY 68 KGASMK-LKPPRPQSTKSPPELRELSRKIRENMKNTISCSARV---NHLPE----- 114
DB 62 ESDVLKVIDQADDTTNAVSIKFFKVTGVTWTTERTDDATVICTRHRIPTLPTEDQII 121
QY 115 -----GHPL--LEKRAEYFHLRLSLKASQGV 137
DB 122 IFQVPIPEPLRFIFPRTEETRTMTHALEEYGV 152

RESULT 36
CREM_CANFA STANDARD; PRT; 344 AA.
AC P79145;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP responsive element modulator.
GN CREM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RX MEDLINE=97410117; PubMed=9266932;
RA Uyttersprot N., Miot F.;
RT "Dog CREM transcription factors: cloning, tissue distribution, and
identification of new isoforms.";
RL Biochem. Biophys. Res. Commun. 237:74-78(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
CC -!- SUBUNIT: Binds DNA as a dimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Beta;
CC IsoId=P79145-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P79145-2; Sequence=Not described;
CC Name=Beta;

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CC      IsoId=P79145-3; Sequence=Not described;
CC      Name=Gamma;
CC      IsoId=P79145-4; Sequence=Not described;
CC      -! PTM: STIMULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC      -! SIMILARITY: Belongs to the BZIP family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X991115; CAA67563.1; -.
CC      PIR; JC5601; JC5601.
CC      InterPro; IPR001630; Leuzip_CREB.
CC      InterPro; IPR003102; PKID.
CC      InterPro; IPR004827; TF_BZIP.
CC      Pfam; PF00170; BZIP; 1.
CC      Pfam; PF02173; PKID; 1.
CC      PRINTS; PR00041; LEUZIPPRCREB.
CC      SMART; SM00338; BRLZ; 1.
CC      PROSITE; PS00217; BZIP; 1.
CC      Transcription regulation; DNA-binding; Activator; Repressor;
CC      Phosphorylation; Nuclear protein; Alternative splicing;
CC      DNA_BIND 287 308 BASIC MOTIF (BY SIMILARITY).
CC      DOMAIN 314 335 LEUCINE-ZIPPER (BY SIMILARITY).
CC      SEQUENCE 344 AA; 36915 MW; 7C50FE323222918 CRC64;
CC      -----
Query Match          9.9%; Score 70; DB 1; Length 344;
Best Local Similarity 23.7%; Pred. No. 37;
Matches 22; Conservative 22; Mismatches 39; Indels 10; Gaps 4;
QY      55 GTGASAIATVTPKGSAMK---LKPEPQSTKSPELRELS-RKIRENMKTTIQESARVN 109
Db      49 GRGSPATVTLVQLPSGQTVHVGIIQTPQSVQIQVATTAETDESAESEGVIDS 108
QY      110 HRLPEGHPLLEKRAEYFRHLRLSKSQ--GVNRL 140
Db      109 HKERE---ILSRPSPYRKILNELSSDPVGPVKI 138
RESULT 37
AIA2-CHICK
ID      AIA2-CHICK STANDARD; PRT; 1017 AA.
AC      F24737;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-MAR-1992 (Rel. 21, Last sequence update)
DE      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Sodium/potassium-transporting ATPase alpha-2 chain (EC 3.6.3.9)
DE      (Sodium pump 2) (Na+/K+ ATPase 2).
GN      ATP1A2.
GC      Gallus gallus (Chicken).
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OC      NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
MEDLINE=91023019; PubMed=2171348;
RA      Takeyasu K., Iamas V., Fambrough D.M.;
RT      "Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.";
RL      Am. J. Physiol. 259:G619-C630(1990).
CC      -! FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME,
CC      WHICH CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF
CC      NA AND K IONS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE
CC      ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR
CC      ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.
CC      -! CATALYTIC ACTIVITY: ATP + H(2)O + Na(+) (In) + K(+) (Out) = ADP +
CC      phosphate + Na(+) (Out) + K(+) (In).
CC      -! SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA

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Db 415 ALSRIAGLCNRAVFKPGQGGNTSISKRDTAGDASESALLKLCIQLSCGVSXKVKRDKNPKVTE 474

Qy 84 SPELRELSRKIRENMKNTSQSARVNHRLPEGHPLLEKRA 123

Db 475 IP-----FNSTYK--YQLSIHEREDPQGHILVMKA 504

RESULT 38

SMC3 YEAST

ID SMC3 YEAST STANDARD; PRT: 1230 AA.

AC P47037;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Structural maintenance of chromosome 3 (DA-Box protein SMC3).

GN SMC3 OR YJL074C OR J1049.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID:4932;

RN SEQUENCE FROM N.A.

RC STRAIN=W303;

RX MEDLINE=97474309; PubMed=9335333;

RA Michaelis C., Ciosk R., Nasmyth K.;

RT "Cohesins: chromosomal proteins that prevent premature separation of sister chromatids";

RL Cell 91:35-45(1997).

RP SEQUENCE FROM N.A.

RA Rose M., Koetter P., Enrian K.D.;

RN Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / FY1678;

RA Sor F.J.;

RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

RN IDENTIFICATION IN A COHESIN COMPLEX WITH SMC1; IRR1 AND MCD1, AND INTERACTION OF THE COHESIN COMPLEX WITH SCC2.

RP INTERACTION OF THE COHESIN COMPLEX WITH SCC2.

RX PubMed=9990856;

RA Toth A., Ciosk R., Uhlmann F., Galova M., Schleiffer A., Nasmyth K.;

RT "yeast Cohesin complex requires a conserved protein, Eco1p(Ctf7), to establish cohesion between sister chromatids during DNA replication.";

RL Genes Dev. 13:320-333(1999).

RN IDENTIFICATION IN A COHESIN COMPLEX WITH SMC3; MCD1 AND IRR1, AND STRUCTURE.

RP PubMed=11983169;

RX Haering C.H., Loewe J., Hochwagen A., Nasmyth K.;

RA "Molecular architecture of SMC proteins and the yeast cohesin complex.";

RT Mol. Cell 9:773-788(2002).

CC -!- FUNCTION: Involved in chromosome cohesion during cell cycle and in DNA repair. Central component of cohesin complex. The cohesin complex is required for the cohesion of sister chromatids after DNA replication. The cohesin complex apparently forms a large proteinaceous ring within which sister chromatids can be trapped. At anaphase, the complex is cleaved and dissociates from chromatin, allowing sister chromatids to segregate.

CC -!- SUBUNIT: Cohesin complexes are composed of the SMC1 and SMC3 heterodimer attached via their hinge domain, MCD1/SCC1 which link them, and IRR1/SCC3, which interacts with MCD1. The cohesin complex also interacts with SCC2, which is required for its association with chromosomes.

CC -!- SUBCELLULAR LOCATION: Nuclear protein. Associates with chromatin. Before prophase it is scattered along chromosome arms. At anaphase, the MCD1 subunit of the cohesin complex is cleaved, leading to the dissociation of the complex from chromosomes, allowing chromosome separation.

CC -!- DOMAIN: The flexible hinge domain, which separates the large intramolecular coiled coil regions, allows the heterotypic interaction with the corresponding domain of SMC1, forming a V-

shaped heterodimer. The two heads of the heterodimer are then connected by different ends of the cleavable MCD1 protein, forming a ring structure (By similarity).

-!- SIMILARITY: Belongs to the SMC family. SMC3 subfamily.

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EMBL: Y14278; CAA74655.1; -

EMBL: Z49349; CAA89366.1; -

EMBL: X88851; CAA61313.1; -

PIR: S56850; S56850.

SGD: S0003610; SMC3.

GO: GO:0007151; P:sporulation (sensu Saccharomycetes); IMP.

GO: GO:0007130; P:synaptonemal complex formation; IMP.

InterPro: IPR003405; SMC_C.

Pfam: PF02463; SMC_N; 1.

Pfam: PF02483; SMC_C; 1.

Mitosis; Cell cycle; Chromosome partition; ATP-binding; Coiled coil; Nuclear protein.

NP_BIND 32 39 ATP (POTENTIAL).

DOMAIN 172 482 COILED COIL (POTENTIAL).

DOMAIN 483 684 FLEXIBLE HINGE.

DOMAIN 685 1041 COILED COIL (POTENTIAL).

DOMAIN 1126 1161 ALA/ASP-RICH (DA-BOX).

SEQUENCE 1230 AA; 141336 MW; B152D88F7780341F CRC64;

Query Match 9.9%; Score 70; DB 1; Length 1230;

Best Local Similarity 25.9%; Pred. No. 1.7e+02;

Matches 29; Conservative 21; Mismatches 42; Indels 20; Gaps 4;

Qy 27 EALLRVKSSERL--AMLRALAGMCGHRVLPCTGASAIATVTPKGASMKLKPFPQSTKS 84

Db 285 EASLKIKNATDLQAKLR-----ESEISQKLT--NVNKKIDVQQQIESN 327

Qy 85 PELREL-SRKIRENMKNTSQSARVNHRLPEGHPLLEKRAEYFRHLASLSQ 135

Db 328 BEQRNLSATLKEIKSIIEQRKQKSLPRYQELTKEEAMYLQLASLOOK 379

RESULT 39

VSIB TRYBB

ID VSIB TRYBB STANDARD; PRT: 471 AA.

AC P07208;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Variant surface glycoprotein ILTAT 1.1BC precursor (VSG).

OS Trypanosoma brucei brucei

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

OX NCBI_TaxID=5702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82245585; PubMed=6927851;

RA "Point mutations during generation of expression-linked extra copy of trypanosome surface glycoprotein gene.";

RL Nature 298:676-679(1982).

CC -!- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE TRYPAOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000 VSG GENES.

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A PI-PLC.

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	D -> G (IN REF. 1).	
	N -> D (IN REF. 1).	
	E -> D (IN REF. 1).	
	KELSKO -> TRRAFEA (IN REF. 1).	
	Q -> H (IN REF. 1).	
	E -> K (IN REF. 1).	
	I -> F (IN REF. 1).	
	A -> P (IN REF. 1).	
	E -> D (IN REF. 1).	
	E -> D (IN REF. 1).	
	L -> V (IN REF. 1).	
	A -> P (IN REF. 1).	
	QSDAEATAARHSFPL -> SKPLRGNSPAFIISF (IN	
	REF. 1).	
	TWILTEDLK -> NRSYDRGLKG (IN REF. 1).	
	A -> S (IN REF. 1).	
	S -> T (IN REF. 1).	
	E -> G (IN REF. 1).	
	A -> S (IN REF. 1).	
	X -> Q (IN REF. 1).	
	L -> Y (IN REF. 1).	
	LQV -> PQF (IN REF. 1).	
	135510 MW; 0163237AAFBCA2B CRC64;	
	9.8%; Score 69.5; DB 1; Length 1186;	
	Best Local Similarity 26.0%; Pred No. 1.e+02;	
	Matches 39; Conservative 22; Mismatches 66; Indels 23; Gaps 7;	
QY	2 ESTSTTNF--VAENRPTFGETF-DVNREALLRVKSSERLAMLRALAGMCGHR-----VLP 54	
	: :	
Db	591 ETAARHSSFGLGASSELVTFDPAYRSVTQNLTGTVLITEDLKGANELAKLLGHRYRIVTL 650	
QY	55 G-----TGASAAIAATVTPKGASMKLKP RPPOSTKSPELRSELSRKIREMNK---TISESAR 107	
Db	651 GDVVNFGSGMTGAVKKQNSL-----LGSRSELEDVTKRLAEEMETALLEQE VKT 702	
QY	108 VNHRLEPGHPLEKRAEYFRHLRSLKSQGV 137	
Db	703 LKHSIODMEKKLADLRETGTGEGLA-LRQQDV 731	

Search completed: November 14, 2003, 10:39:23
Job time : 39 secs

OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:35 ; Search time 68 Seconds

(without alignments)
535.080 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 708

Sequence: 1 MESTSTTNFVAENRPTFGE.....RAEYFRHLRLSLKSGQVNRLLI 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	141	5 Q8MN4	Q8MN4 babesia can
2	603	85.2	285	5 Q8MQH4	Q8MQH4 babesia can
3	87.5	12.4	610	13 Q91431	Q91431 xenopus lae
4	85	12.1	524	16 Q9RV10	Q9RV10 deinoxoccus
5	85	12.0	478	16 Q8PDC3	Q8PDC3 xanthomonas
6	84.5	11.9	609	13 Q92021	Q92021 xenopus lae
7	83	11.7	192	15 Q56002	Q56002 human immun
8	83	11.7	1053	4 Q95625	Q95625 homo sapien
9	82	11.6	192	15 Q55997	Q55997 human immun
10	82	11.6	192	15 Q78242	Q78242 human immun
11	82	11.6	192	15 Q56010	Q56010 human immun
12	82	11.6	192	15 Q56006	Q56006 human immun
13	82	11.6	239	16 Q8FVGS	Q8FVGS anabaena sp
14	82	11.6	291	2 Q93T00	Q93T00 acidithioba
15	82	11.6	988	10 P93661	P93661 chenopodium
16	81.5	11.5	378	11 Q8R089	Q8R089 mus musculus

17	81.5	11.5	1281	16 Q91211	Q91211 pseudomonas
18	81	11.4	192	15 Q55960	Q55960 human immun
19	81	11.4	192	15 Q56000	Q56000 human immun
20	81	11.4	192	15 Q56005	Q56005 human immun
21	81	11.4	192	15 Q79079	Q79079 human immun
22	80.5	11.4	412	4 Q8NHV2	Q8NHV2 homo sapien
23	80.5	11.4	448	4 Q8NA61	Q8NA61 homo sapien
24	80.5	11.4	452	16 Q93IX7	Q93IX7 streptomyce
25	80.5	11.4	1157	5 Q3VP22	Q3VP22 drosophila
26	80.5	11.4	1157	5 Q8T9E1	Q8T9E1 drosophila
27	80	11.3	192	15 Q56008	Q56008 human immun
28	80	11.3	192	15 Q91QF2	Q91QF2 human immun
29	80	11.3	464	16 Q910T6	Q910T6 pseudomonas
30	80	11.3	819	13 Q9YHC1	Q9YHC1 perca flave
31	80	11.3	895	13 Q9WGN1	Q9WGN1 perca flave
32	80	11.3	902	10 Q81209	Q81209 arabidopsis
33	80	11.3	902	10 Q8LY21	Q8LY21 arabidopsis
34	80	11.3	1017	2 Q8VW43	Q8VW43 bradyrhizob
35	79.5	11.2	211	5 Q9Y069	Q9Y069 periplaneta
36	79.5	11.2	348	10 Q8VYQ4	Q8VYQ4 arabidopsis
37	79.5	11.2	357	16 Q9RKL6	Q9RKL6 streptomyce
38	79.5	11.2	4065	3 Q9P421	Q9P421 neurospora
39	79	11.2	192	15 Q9YB41	Q9YB41 human immun
40	79	11.2	192	15 Q79093	Q79093 human immun
41	79	11.2	192	15 Q79105	Q79105 human immun
42	79	11.2	192	15 Q56009	Q56009 human immun
43	79	11.2	192	15 Q73459	Q73459 human immun
44	79	11.2	192	15 Q9WP97	Q9WP97 human immun
45	79	11.2	192	15 Q56004	Q56004 human immun

ALIGNMENTS

RESULT 1

Q8MN4 PRELIMINARY; PRT; 141 AA.
 ID Q8MN4
 AC Q8MN4
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DE Putative vir15 protein.
 GN VIR.
 OS Babesia canis.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
 OX NCBI_TaxID=5867;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Drakulovski P., Carcy B., Moubri K., Carret C., Depoix D.,
 RA Schetters T.P.M., Gorenflot A.;
 RT "An extrachromosomal dsRNA from Babesia canis implicated in parasite virulence";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ494862; CAD41951.1; --
 SQ SEQUENCE 141 AA; 15752 MW; B84419C128FD7CD1 CRC64;

Query Match	100.0%;	Score 708;	DB 5;	Length 141;
Best Local Similarity	100.0%;	Pred. No. 2.5e-59;		
Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MESTSTTNFVAENRPTFGETFDVNR	REALLRVKSSERLAMLRLALAGMCGH	RVLPQTGASA 60
DB	1	MESTSTTNFVAENRPTFGETFDVNR	REALLRVKSSERLAMLRLALAGMCGH	RVLPQTGASA 60
QY	61	IAATVTPKGASMKLPPRPQSTKSP	ELSRKIRKIRKNTISQESARVNHRL	PEGHPLLE 120
DB	61	IAATVTPKGASMKLPPRPQSTKSP	ELSRKIRKIRKNTISQESARVNHRL	PEGHPLLE 120
QY	121	KRAEYFRHLRLSLKSGQVNRLLI	141	
DB	121	KRAEYFRHLRLSLKSGQVNRLLI	141	

```
RESULT 2
Q8MQH4 PRELIMINARY; PRT; 285 AA.
ID AC Q8MQH4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Putative vir32 protein.
GN VIR.
OS Babesia canis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5867;
RN [1]
RP SEQUENCE FROM N.A.
RA Drakulovski P., Carcy B., Moubri K., Carret C., Depoix D.,
RA Schettlers T.P.M., Gorenflot A.;
RT "An extrachromosomal dsRNA from Babesia canis implicated in parasite
RL virulence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ494862; CAD41950.1;
SQ SEQUENCE 285 AA; 32169 MW; 45ACEFEC7927243D CRC64;

Query Match 85.2%; Score 603; DB 5; Length 285;
Best Local Similarity 90.4%; Pred. No. 5e-49;
Matches 122; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MESTSTTNFVAENRPTFGTFTDVMREALLRVKSSERLAMLALAGVCGHRVLPGTGASA 60
DB 1 MESTSTTNFVAENRPTFGTFTDVMREALLRVKSSERLAMLALAGVCGHRVLPGTGASA 60
QY 61 IATVTPKGSMLKPPRPOSTKSPPELRSLKIRENMKTIQESARVNHRLPEGHPLLE 120
DB 61 IATVTPKGSMLKPPRPOSTKSPPELRSLKIRENMKTIQESARVNHRLPEGHPLLR 120
QY 121 KRAEYFRHLRLSLK 135
DB 121 SGQNIFVTLDLRAK 135

RESULT 3
Q91431 PRELIMINARY; PRT; 610 AA.
ID AC Q91431;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Nuclear factor 7.
GN XNF7-O.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Gong S.G., Reddy B.A., Etkin L.D.;
RT "Two forms of Xenopus nuclear factor 7 have overlapping spatial but
RT different temporal patterns of expression during development.";
RL Mech. Dev. 52:305-318(1993)
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: S80988; AAB35876.1;
DR InterPro: IPR001870; B302.
DR InterPro: IPR003649; Bbox C.
DR InterPro: IPR000953; Chromo.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY receptor.
DR InterPro: IPR003015; Znf Bbox.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00622; SPRY; 1.
DR Pfam: PF00643; zf-B_box; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART; SMC0502; BBC; 1.
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DR SMART; SMC0336; BBOX; 1.
DR SMART; SMC0298; CHROMO; 1.
DR SMART; SMC0589; PRY; 1.
DR SMART; SMC0184; RING; 1.
DR SMART; SMC0449; SPRY; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS00518; ZF_RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 610 AA; 69115 MW; D828F6060572EC1 CRC64;

Query Match 12.4%; Score 87.5; DB 13; Length 610;
Best Local Similarity 32.0%; Pred. No. 7.3;
Matches 31; Conservative 12; Mismatches 37; Indels 17; Gaps 4;

QY 50 HRVLP-----GTGASAIATVTPKGSMLKPPRPOSTKSPPELR-ELSRKIRENMKTIQ 103
DB 256 HNFILPILDAIGYIRELSAIVAPLEASLKV-----TEQLSGEQSDKIEQHNNKVSQ 306
QY 104 ESARNVHRLPEGHPLLEKRAEYFRHLRLSLKSGQVNRLL 140
DB 307 YKEHTVSEFEKLHFLKEREE--KLLEQLKEQGDNLL 341

RESULT 4
Q9RY10 PRELIMINARY; PRT; 524 AA.
ID AC Q9RY10;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Protein kinase, putative.
GN DRA0332.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.J., Uitterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI.".
RL Science 286:1571-1577(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AE001863; AAF12449.1;
DR TIGR; DRA0332;
DR InterPro: IPR000719; Prot Kinase.
DR InterPro: IPR002965; P-rich exten.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00669; pkinase; 1.
DR PRINTS; PR01217; PRICHEXTENSN.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
KW Complete proteome.
SQ SEQUENCE 524 AA; 55298 MW; 79807356B6BE2AED CRC64;

Query Match 12.1%; Score 86; DB 16; Length 524;
Best Local Similarity 29.0%; Pred. No. 8.5;
Matches 29; Conservative 23; Mismatches 28; Indels 20; Gaps 6;

QY 25 MREALL-----RVKSSERLAMLALAGVCGHRVLPGTG-----ASAIATVTPKGSMLK 75
DB 256 HNFILPILDAIGYIRELSAIVAPLEASLKV-----TEQLSGEQSDKIEQHNNKVSQ 306
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Db 287 LREAVLSMAPRIENRQSA--QAL-----RRILRGEGTVTAAAPAAPOPOQSPVR 339

Qy 76 P---PRQSTKSPEL-RELSKIREMKTISQSAVNHR 111

Db 340 PSPAPTTPNPQTDREVEKRLRELEKEVRKARQSR 379

RESULT 5

Q8PDC3 PRELIMINARY; PRT; 478 AA.

AC Q8PDC3;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein XC0417.

GN XC0417.

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=2202145; PubMed=1204217;

RA da Silva A.C.R., Ferio J.A., Reinach P.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Cicarotte G., Cannavan F., Cardoso J., Chamberg F., Ciapina L.P.,

RA Cicaralli R.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Tundade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Secubal J.C., Kitajima J.P.,

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RL Nature 417:459-463(2002).

DR EMBL; AE012139; AAM39735.1; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 478 AA; 51984 MW; 9A239F7950580A89 CRC64;

Query Match 12.0%; Score 85; DB 16; Length 478;

Best Local Similarity 29.7%; Pred. No. 9.4;

Matches 27; Conservative 16; Mismatches 38; Indels 10; Gaps 3;

Qy 49 GHR-----VLPTGASATAATVTPKGSMKLPKPPRQSTKSPKELSKIREMKTISQ 104

Db 216 GHRGLLAISRGAPQAHLRQP-GRALPPHLQRAIKADLRALLRGVRLSVVVDW 274

Qy 105 SARVNHRLPEGHPL-----LEKRAEYFRHLR 130

Db 275 RRVVDALRPHLPQWQRLSQARFLHLR 305

RESULT 6

Q92021 PRELIMINARY; PRT; 609 AA.

AC Q92021;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE XNF7=ZINC finger nuclear phosphoprotein.

GN XNF7.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92038424; PubMed=1936552;

RA Reddy B.A., Kloc M., Etkin L.;

RT "The cloning and characterization of a maternally expressed novel zinc

RT finger nuclear phosphoprotein (xnf7) in Xenopus laevis.";

RL Dev. Biol. 148:107-116(1991).

RN [2]

RP SEQUENCE FROM N.A.

RA Reddy B.A., Kloc M., Etkin L.D.;

RL Submitted (APR-1991) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; S64515; AAB20269.1; -

DR EMBL; M63705; AAA49995.1; -

DR InterPro; IPR001870; B302.

DR InterPro; IPR000953; Chromo.

DR InterPro; IPR006574; PRY.

DR InterPro; IPR003877; SPRY receptor.

DR InterPro; IPR000315; Znf Bbox.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00622; SPRY; 1.

DR Pfam; PF00643; Zf-B_box; 1.

DR Pfam; PF00097; Zf-C3HC4; 1.

DR SMART; SM00336; BBOX; 1.

DR SMART; SM00298; CHROMO; 1.

DR SMART; SM00589; PRY; 1.

DR SMART; SM00184; RING; 1.

DR SMART; SM00449; SPRY; 1.

DR PROSITE; PS00119; ZF_BBOX; 1.

DR PROSITE; PS00518; ZF_RING_1; 1.

DR PROSITE; PS00089; ZF_RING_2; 1.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 609 AA; 68875 MW; 088C8312B45C78F8 CRC64;

Query Match 11.9%; Score 84.5; DB 13; Length 609;

Best Local Similarity 30.9%; Pred. No. 14;

Matches 30; Conservative 12; Mismatches 38; Indels 17; Gaps 4;

Qy 50 HRVLP-----GTGASATAATVTPKGSMKLPKPPRQSTKSPKEL-RELSKIREMKTISQ 103

Db 255 HNFPLTDAVGVRBELSAIVAPLEASLKV-----TEQLSSEQSDKIEOHKNMSQ 305

Qy 104 ESARVNHRLPEGHPLLEKRAEYFRHLRLSKISQGVNRL 140

Db 306 YKEHITSEFKLHLRERE--KULEQLKEQGENLL 340

RESULT 7

O56002 PRELIMINARY; PRT; 192 AA.

AC O56002;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Vif protein (Vifon infectivity factor) (SOR protein).

GN VIF.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EI08;

RX MEDLINE=98105749; PubMed=9445004;

RA Yedavalli V.R., Chappey C., Matala E., Ahmad N.;

RT "Conservation of an intact vif gene of human immunodeficiency virus

RT type 1 during maternal-fetal transmission.";

RL J. Virol. 72:1092-1102(1998).

CC -1- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).

DR EMBL; AF019511; AAC02385.1; -

DR InterPro; IPR000475; Viral_infect.

DR Pfam; PF00559; Vif; 1.

DR PRINTS; PR00349; VIRIONINFECT.

DR ProDom; PD000063; Viral_infect; 1.

KW AIDS.
SQ SEQUENCE 192 AA; 22545 MW; FE30C8963FFOE79 CRC64;
Query Match 11.7%; Score 83; DB 15; Length 192;
Best Local Similarity 28.8%; Pred. No. 4.8;
Matches 30; Conservative 10; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDMREALLRVKSSRLAMRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
DB 112 FDCFSSEAIR-----KALLGHRVSPRCNYQAGHNKVGSLQYKALAALIKPK--- 157
QY 73 KLPKPPRPOSTKSPELRSKIREMKNKTISOESARVNHRLPEGH 116
DB 158 KIKPLPSVTKLTEDR-----WNKPKQTKGHRGNHTM-DGH 192
RESULT 8
O95625 PRELIMINARY; PRT; 1053 AA.
ID O95625
AC O95625
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang C.M., Seto E.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U69274; AAD00172.1; -
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00651; BTB; 1
DR Pfam; PF00096; Zf_C2H2; 12.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00355; Znf_C2H2; 12.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 12.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 1053 AA; 119382 MW; C7BJC518534BF2D6 CRC64;
Query Match 11.7%; Score 83; DB 4; Length 1053;
Best Local Similarity 25.4%; Pred. No. 38;
Matches 34; Conservative 18; Mismatches 66; Indels 16; Gaps 5;
QY 9 NFVAENRPT-FGETFDVNRALLRVKSSERLAMLALAGM---CGHRVLPGTGASAI 63
DB 486 NLVASTAKTNGPDDTYR-SRLQRSVNEGAYIRLHKGMKKLQKRAVFKSAVQVQAQ 544
QY 64 TVTPKGAMKLPKPPRPOSTKSPELRSKIREMKNKTISOESARVNHRLPEGH-----P 117
DB 545 KLVQRGKKVK---QPKRDAXENTEEASHKCGCGVFFQRYALIMHKLKHERADYKCP 600
QY 118 LLEKRAEYFRHLRS 131
DB 601 LCKKQFQVSASLRA 614
RESULT 9
O55997 PRELIMINARY; PRT; 192 AA.
ID O55997
AC O55997
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BI03.
RX MEDLINE=98105749; PubMed=9445004;
RA Yedavalli V.R., Chappey C., Matala E., Ahmad N.;
RT "Conservation of an intact vif gene of human immunodeficiency virus
type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -I- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019506; AAC02380.1; -
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22574 MW; 37F3A1B988F1FAB0 CRC64;
Query Match 11.8%; Score 82; DB 15; Length 192;
Best Local Similarity 28.0%; Pred. No. 6;
Matches 30; Conservative 9; Mismatches 30; Indels 38; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLALAGMCGHRVLPGTGAS-----KALLGHRVSPRCNYQAGHNKVGSLQYKALAALIKPK- 157
DB 112 FDCFSSEAIR-----KALLGHRVSPRCNYQAGHNKVGSLQYKALAALIKPK- 157
QY 70 ASMKLAPPRPOSTKSPELRSKIREMKNKTISOESARVNHRLPEGH 116
DB 158 ---KIKPLPSVTKLTEDR-----WNKPKQTKGHRGNHTM-DGH 192
RESULT 10
Q78242 PRELIMINARY; PRT; 192 AA.
ID Q78242
AC Q78242
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,
RA Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer
chronically infected HUT-78 cellular clone.";
RL J. Viral Diseases 1:40-55(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federic M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
producer clones from HUT-78 infected with a patient HIV isolate.";
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Borsetti A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
CC -I- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; Z11530; CAA77623.1; -
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22543 MW; 485E434FC92CCAD6 CRC64;

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Query Match 11.6%; Score 82; DB 15; Length 192;
Best Local Similarity 28.8%; Pred. No. 6;
Matches 30; Conservative 9; Mismatches 33; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLALAG-----MCHRVLPOTGASATAATVTPKGSM 72
DB 112 FDCFSASIR-----NAILGNVRLSCYQAGHNKIGSLQYLALALAIKPK-----157
QY 73 KLKPPRPQSTKSPPELRELSRKIREMKNKTISQESARVNHRLPEGH 116
DB 158 KIKPPLPSVTKLTEDR-----WNKPQKTGHRGNHTM-NGH 192

RESULT 11
OS6010 PRELIMINARY; PRT; 192 AA.
AC OS6010;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Vif protein (Virion infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=EM05.
RX MEDLINE=98105749; PubMed=9445004;
RA Yedavalli V.R., Chappey C., Matala E., Ahmad N.;
RT "Conservation of an intact vif gene of human immunodeficiency virus
RT type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL: AF019521; AAC02389.1; -.
DR InterPro: IPR000475; Viral_infect.
DR Pfam: PF00559; Vif; 1.
DR PRINTS: PR00349; VIRIONINFCT.
DR ProDom: PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22618 MW; 1BDB93032900D1E CRC64;

Query Match 11.6%; Score 82; DB 15; Length 192;
Best Local Similarity 28.8%; Pred. No. 6;
Matches 30; Conservative 10; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLALAG-----MCHRVLPOTGASATAATVTPKGSM 72
DB 112 FDCFSASIR-----KALLGHRVSPRCDYQAGHNWGSLOYLALALAIKPK-----157
QY 73 KLKPPRPQSTKSPPELRELSRKIREMKNKTISQESARVNHRLPEGH 116
DB 158 KIKPPLPSVTKLTEDR-----WNKPQKTGHRGNHTM-NGH 192

RESULT 12
OS6006 PRELIMINARY; PRT; 192 AA.
AC OS6006;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Vif protein (Virion infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN=EI12.
RX MEDLINE=98105749; PubMed=9445004;
RA Yedavalli V.R., Chappey C., Matala E., Ahmad N.;
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RT "Conservation of an intact vif gene of human immunodeficiency virus
RT type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL: AF019515; AAC02389.1; -.
DR InterPro: IPR000475; Viral_infect.
DR Pfam: PF00559; Vif; 1.
DR PRINTS: PR00349; VIRIONINFCT.
DR ProDom: PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22572 MW; FD01CC0B85E4B0BD CRC64;

Query Match 11.6%; Score 82; DB 15; Length 192;
Best Local Similarity 28.0%; Pred. No. 6;
Matches 30; Conservative 9; Mismatches 30; Indels 38; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLALAGMCHRVLPOTGAS-----NIAATVTPKG 69
DB 112 FDCFSASIR-----KALLGHRVSPRCNYQAGHNKVGSLQYLALALAIKPK-157
QY 70 ASMKLKPPRPQSTKSPPELRELSRKIREMKNKTISQESARVNHRLPEGH 116
DB 158 ---KIKPPLPSVTKLTEDR-----WNKPQKTGHRGNHTM-DGH 192

RESULT 13
Q8YVGS PRELIMINARY; PRT; 239 AA.
AC Q8YVGS;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical protein A112013.
GN A112013.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003587; BAB73712.1; -.
DR InterPro: IPR001601; Methyltransf.
DR ProDom: PD000051; SAM_bind.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 239 AA; 26707 MW; 71345D5EC7FDEB66 CRC64;

Query Match 11.6%; Score 82; DB 16; Length 239;
Best Local Similarity 26.9%; Pred. No. 7.8;
Matches 21; Conservative 16; Mismatches 39; Indels 2; Gaps 1;

QY 61 IAATVTPKGASMKLKPPOSTKSPPELRELSRK---IREMKNKTISQESARVNHRLPEGHPL 118
DB 141 IAASLTENGCFWNADPLPSPTLAEIYQARBEMVSEQSNFTEVRAKYDSDSPQYSN 200
QY 119 LEKRAEYFRHLRLSKSQG 136
DB 201 PDQLATLDTLQMLTKSG 218

RESULT 14
Q93TU0 PRELIMINARY; PRT; 291 AA.
AC Q93TU0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
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DT	01-DEC-2001 (T-EMBLrel. 19, Last annotation update)	
DE	Helicase-like protein.	
GN	REPA.	
OS	Acidithiobacillus caldus.	
OG	Plasmid pTC-F14.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.	
OX	NCBI_TaxID=33059;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=2124728; Pubmed=11344137;	
RT	Gardner M.N.; Deane S.M.; Rawlings D.E.;	
RA	"Isolation of a New Broad-Host-Range IncQ-Like Plasmid, pTC-F14, from	
RT	the Acidophilic Bacterium Acidithiobacillus caldus and Analysis of the	
RT	Plasmid Replicon."	
RL	J. Bacteriol. 183:3303-3309 (2001).	
RL	EMBL; AF325537; AAK56915.1; -.	
KW	Plasmid	
QY	SEQUENCE 291 AA; 31324 MW; DB726E4864C7609B CRC64;	
QY	Query Match 11.6%; Score 82; DB 2; Length 291;	
QY	Best Local Similarity 23.4%; Pred. No. 9.9;	
QY	Matches 33; Conservative 26; Mismatches 56; Indels 24; Gaps 5;	
QY	11 VAEN---RPTFGTFFDVMREA---LLRVKSSERLAMLRLALA-----GNCGH--- 50	
DB	101 I AENLTLEPIMGKELNIMDEAHLHRIIEASGARLIVDTLSRIHNLDNSNGMAHLVA 160	
QY	51 ---RVLPGTGASIAAATVTPKGSAMKMLKPPRPOSTK-SPELRELSRKIRENKTIQSESA 106	
DB	161 TLEHIAASTGASVLYLHVHSGKSGMAGQTDQQAARGASALIDNARCGYVAKVAEHA 220	
QY	107 RVNHLRPEGHPLLEKRAEYFR 127	
DB	221 RLSDRSFDRAPIGDRRGFFVR 241	
QY	RESULT 15	
QY	P93661 PRELIMINARY; PRT; 988 AA.	
AC	P93661;	
DT	01-MAY-1997 (T-EMBLrel. 03, Created)	
DT	01-MAY-1997 (T-EMBLrel. 03, Last sequence update)	
DT	01-DEC-2001 (T-EMBLrel. 19, Last annotation update)	
DE	Mitochondrial single-subunit DNA-dependent RNA polymerase.	
OS	Chenopodium album (lamb's-quarters).	
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
OC	Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.	
OX	NCBI_TaxID=3559;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=97315321; Pubmed=9171081;	
RA	Weihe A.; Hedtke B.; Boerner T.;	
RT	"Cloning and characterization of a cDNA encoding a bacteriophage-type	
RT	RNA polymerase from the higher plant Chenopodium album."	
RL	Nucleic Acids Res. 25:2319-2325 (1997).	
RL	EMBL; Y08067; CAA69305.1; -.	
DR	HSSP; P00573; IARO.	
DR	InterPro; IPR02092; RNA_pol_phase.	
DR	Pfam; PF00940; RNA_pol_1.	
DR	PROSITE; PS00900; RNA_POL_PHAGE_1; 1.	
DR	PROSITE; PS00489; RNA_POL_PHAGE_2; 1.	
QY	SEQUENCE 988 AA; 111854 MW; 65B5496C425D31A9 CRC64;	
QY	Query Match 11.6%; Score 82; DB 10; Length 988;	
QY	Best Local Similarity 25.9%; Pred. No. 44;	
QY	Matches 29; Conservative 17; Mismatches 52; Indels 14; Gaps 3;	
QY	11 VAENRPTFGTFFDVMREALLRVKSSERLAMLRLALACMGCHRVLPCTGASIAAATVTPKGA 70	
DB	216 VGENRPLYGCTDFELPADMAVITMKMLGL-----WTG-----SGNGGTTVIOAAQTIGE 267	
QY	71 SMKLKPPRPOSTKSPELRELSRKIRENKTIQSESARVNHLRPEGHPLLEKR 122	

QY 25 MBEALLRVKSSER-LA-----MLRALAGMCGHRVLPGTGASAIATVTPKGASMKLXPPRP 79
Db 743 LREQLLARELDQLADTGEALLAGLAGRFVAPGGDFINPQVPSGRNLFAP---- 798
QY 80 QSTKSPRELRSKIREMKNKTISOESARVNH--RLPEGHPLLEKRAEYFRHLFSLKXSGV 137
Db 799 EADKVPTRAAVEAGAEAFGLL--ESVRAEHQGRAPEKLAFLWSSETMRLHLGIVESQAL 856
QY 138 NRL 140
Db 857 HAL 859

RESULT 18
ID O55960 PRELIMINARY; PRT; 192 AA.
AC O55960;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BI12;
RX MEDLINE=98105749; PubMed=9445004;
RA Yedavalli V.R., Chappey C., Matala E., Ahmad N.;
RT "Conservation of an intact vif gene of human immunodeficiency virus
type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019458; AAC02338.1; -;
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22410 MW; D841DA0216CC54AB CRC64;

Query Match 11.4%; Score 81; DB 15; Length 192;
Best Local Similarity 27.6%; Pred. No. 7.4;
Matches 29; Conservative 12; Mismatches 32; Indels 32; Gaps 5;
QY 21 TFDVMEALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGAS 71
Db 111 SDFCFSESAR-----NAILGRVIRPSCDFQAGHNKVGSLQYLALALITPK--- 157
QY 72 MKLKPVRPQSTKSPRELRSKIREMKNKTISOESARVNHRLPEGH 116
Db 158 -KIKPPLPSVAKLTEDR-----WNKPQTKGSRGSHRM-NGH 192

RESULT 19
ID O56000 PRELIMINARY; PRT; 192 AA.
AC O56000;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EI06;
RX MEDLINE=98105749; PubMed=9445004;
RA Yedavalli V.R., Chappey C., Matala E., Ahmad N.;

RT "Conservation of an intact vif gene of human immunodeficiency virus
type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019509; AAC02383.1; -;
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22473 MW; 707084D505264482 CRC64;

Query Match 11.4%; Score 81; DB 15; Length 192;
Best Local Similarity 28.0%; Pred. No. 7.4;
Matches 30; Conservative 8; Mismatches 31; Indels 38; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLALAGMCGHRVLPGTGAS-----AIAATVTPKG 69
Db 112 FDCFSESAIR-----KALLGHRVSPRCYQAGHNKVGSLQYLALALIKPK- 157
QY 70 ASMKLKPVRPQSTKSPRELRSKIREMKNKTISOESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGHRGNHTM-NGH 192

RESULT 20
ID O56005 PRELIMINARY; PRT; 192 AA.
AC O56005;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EI11;
RX MEDLINE=98105749; PubMed=9445004;
RA Yedavalli V.R., Chappey C., Matala E., Ahmad N.;

RT "Conservation of an intact vif gene of human immunodeficiency virus
type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019514; AAC02388.1; -;
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22428 MW; 62F54F070104CDE7 CRC64;

Query Match 11.4%; Score 81; DB 15; Length 192;
Best Local Similarity 28.0%; Pred. No. 7.4;
Matches 30; Conservative 8; Mismatches 31; Indels 38; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLALAGMCGHRVLPGTGAS-----AIAATVTPKG 69
Db 112 FDCFSESAIR-----KALLGHRVSPRCYQAGHNKVGSLQYLALALIKPK- 157
QY 70 ASMKLKPVRPQSTKSPRELRSKIREMKNKTISOESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGHRGNHTM-NGH 192

RESULT 21
ID Q79079 PRELIMINARY; PRT; 192 AA.
AC Q79079;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif (viral infectivity factor) (Viron infectivity factor) (SOR
DE protein).
GN Vif.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94303241; PubMed=8030283;
RA Wieland U., Hartmann J., Suhr H., Salzberger B., Eggers HJ.,
RA Kuehn J.E.;
RT "In vivo genetic variability of the HIV-1 vif gene."
RL Virology 203:43-51(1994).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; Z30687; CA83167.1; -
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1
DR PRINTS; PR00349; VIRIONINFECT.
DR PRODOM; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22529 MW; 20CD70E9953B8DCC CRC64;

Query Match 11.4%; Score 81; DB 15; Length 192;
Best Local Similarity 29.8%; Pred. No. 7.4;
Matches 31; Conservative 8; Mismatches 33; Indels 32; Gaps 5;
Qy 22 PDVREALLRVKSSERLAMLALAG-----MCHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCSESAIR-----KAILGHIVSPCEYQAGHNKVGSLQYLALAAALVTPK--- 157
Qy 73 KLKPPPOSTKSPPELRELSRKIREMNKTIQESARVNHRLPEGH 116
Db 158 KTKPLPSVTKLTEDR-----WNKPKQTKGHNHTM--NGH 192

RESULT 22
Q8NHV2
ID Q8NHV2 PRELIMINARY; PRT; 412 AA.
AC Q8NHV2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to RIKEN CDNA 1700086N05 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027609; AAH27609.1; -
SQ SEQUENCE 412 AA; 47288 MW; 65C3B47EF08CDE10 CRC64;

Query Match 11.4%; Score 80.5; DB 4; Length 412;
Best Local Similarity 29.8%; Pred. No. 21;
Matches 28; Conservative 15; Mismatches 42; Indels 9; Gaps 3;
Qy 48 CGHRVLPGTGASAIATVTPKGASMKLPPRPQSTKSPPELRELSRKIREMNKTIQESAR 107
Db 256 CSPGLLDQSGLSRPEEPKG-----PPARQE-DSKELRALRKQVSNMGSFGSEEEK 308
Qy 108 VNHRLPGLHPLLEKRAEYFRHLRSLSKSGVNRLL 141
Db 309 VGPGLPDGCQPLQLLRMRQALQALLKE--NRLL 340

RESULT 23
Q8NA61
ID Q8NA61 PRELIMINARY; PRT; 448 AA.
AC Q8NA61;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ35810.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Oshima A., Takahashi-Fujii A., Tanase T., Inose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Naganari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK093129; BAC04067.1; -
KW Hypothetical protein.
SQ SEQUENCE 448 AA; 51570 MW; D59271CFE59F8863 CRC64;

Query Match 11.4%; Score 80.5; DB 4; Length 448;
Best Local Similarity 29.8%; Pred. No. 23;
Matches 28; Conservative 15; Mismatches 42; Indels 9; Gaps 3;
Qy 48 CGHRVLPGTGASAIATVTPKGASMKLPPRPQSTKSPPELRELSRKIREMNKTIQESAR 107
Db 292 CSPGLLDQSGLSRPEEPKG-----PPARQE-DSKELRALRKQVSNMGSFGSEEEK 344
Qy 108 VNHRLPGLHPLLEKRAEYFRHLRSLSKSGVNRLL 141
Db 345 VGPGLPDGCQPLQLLRMRQALQALLKE--NRLL 376

RESULT 24
Q93IX7
ID Q93IX7 PRELIMINARY; PRT; 452 AA.
AC Q93IX7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SC01293.
GN SC01293 OR SCBAC36F5.04.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;

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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K.S., Pollard D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Poulack J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zavazzi J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2165-2195(2000)
RL
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AE003594; AAFL5138.1; -.
DR RSSP; P24941; LHCL.
DR DR Flybase; FBgn0037093; CG7597.
DR InterPro; IPRO00719; Prot kinase.
DR InterPro; IPRO02290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc_1
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ KW SEQUENCE 1157 AA; 128332 MW; B37ADCFBCAB4E9F3 CRC64;

Query Match 11.4%; Score 80.5; DB 5; Length 1157;
Best Local Similarity 28.4%; Pred.No.73;
Matches 25; Conservative 13; Mismatches 37; Indels 13; Gaps 3;

QY 55 GTGASAJAATVTPKGAS--MKUKPPRP-----QSTKSPELNELSR--KIREMNKI 101
DB |||| :|: |:| | | | | | | | | | | | | | | | | | | | | | | | |
462 GTGTSGDYSRSRPTSSRYMESSPPSVGASGHYHRRSRPMQRQTGRDSRRRSSSA 521

QY 102 SCESARNVHLPEGHPLLEKRAEYFRHL 129
DB |||| | | | | | | | | | | | | | | | | | | | | | | | | | |

522 SSEASASRSRPTSRDLKHREVIYIKI 549
DB |||| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 26
QB9T9EI PRELIMINARY; PRT; 1157 AA.
AC QB9T9EI;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SD04681p.
OS Drosophila melanogaster [fruit fly].
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDJB databases.
RL -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC EMBL; AY069806; AALJ3951.1; -.
DR RSSP; P24941; IEUH.
DR DR Flybase; FBgn0037093; CG7597.
DR InterPro; IPRO00719; Prot kinase.
DR InterPro; IPRO02290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11676;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20338596; PubMed=10881687;
 RY Yamada T., Iwamoto A.;
 RA "Comparison of proviral accessory genes between long-term
 RT nonprogressors and progressors of human immunodeficiency virus type 1
 RT infection.";
 RL Arch. Virol. 145:1021-1027(2000).
 CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
 CC EMBL: AB034482; BAA93939.1; -;
 DR InterPro; IPR000475; Viral_infect.
 DR Pfam; PF00559; Vif; 1.
 DR PRINTS; PR00349; VIRIONINFFCT.
 DR ProDom; PD000063; Viral_infect; 1.
 KW AIDS.
 SQ SEQUENCE 192 AA; 22662 MW; 57211D37DEFB0F95 CRC64;
 Query Match 11.3%; Score 80; DB 15; Length 192;
 Best Local Similarity 30.8%; Pred.No.9.2;
 Matches 32; Conservative 7; Mismatches 33; Indels 32; Gaps 5;
 QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCHRVLPGTGSAIAATVTPKGSM 72
 DB 112 FDFSESAR-----RALLGKIVSPSCYQAGTKRVFLYALALALVTPK---- 157
 QY 73 KLPKPPQSTKSPELRELSRKIREMKNKTSQESARVNHRLPEGH 116
 DB 158 KIKPPLPSVAKLTEDR-----WNKPKTKGHRGNHTM-NGH 192
 RESULT 29
 Q91076 PRELIMINARY; PRT; 464 AA.
 ID Q91076
 AC Q91076;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Hypothetical protein PA2548.
 GN PA2548.
 OS Pseudomonas aeruginosa.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 CX NCBI_TaxID=287;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC 15692 / PAO1;
 RC MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 RL EMBL: AE004682; AG05936.1; -;
 DR InterPro; IPR006685; OmpA/MotB.
 DR Pfam; PF00691; OmpA; 1.
 DR ProDom; PD000930; OmpA/MotB; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 464 AA; 51031 MW; 4F4BE8280F0820D7 CRC64;
 Query Match 11.3%; Score 80; DB 16; Length 464;
 Best Local Similarity 27.5%; Pred.No.27;
 Matches 36; Conservative 17; Mismatches 46; Indels 32; Gaps 7;
 QY 20 ETDVNVREALLRVKSSERLAMLRLALAGMCHRVLPGTGSAIAATVTPKG-ASMKLK--- 75
 DB 285 EDPFLGRRFLYIKPKGKNPWAQV-----RPAQGPGRGAI---VTRSGFVAQKIQAVQ 336

QY 76 -PPRQSTKSPBLRSLKIREMNTISQESARVNHRLPEGHPLLEKKA-----EYF 126
DB 337 IAPRPQ-MPAEYRLAEQARRLT-----VNFREFQSALLDNKALLDQVRLLDYL 385
QY 127 RHLRSLSKQGV 137
DB 386 RQNRKLQERTV 396

RESULT 30
Q9YHCL1 PRELIMINARY; PRT; 819 AA.
AC Q9YHCL1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lysyl oxidase-like protein (Fragment).
GN PLO1.
OS Perca flavescens (Yellow perch).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Percidae; Perca.
OX NCBI_TaxID=8167;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Langenau D.M., Goetz F.W., Roberts S.B.;
RT "Progestin-upregulated mRNAs in the yellow perch ovary."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103901; AAC79085.2; -
DR InterPro; IPR001695; Lysyl oxidase.
DR InterPro; IPR001190; Srcr receptor.
DR Pfam; PF01186; Lysyl oxidase; 1.
DR Pfam; PF00530; SRCR; 4.
DR PRINTS; PR00074; LYSYLOXIDASE.
DR ProDom; PD013887; Lysyl oxidase; 1.
DR SMART; SM00202; SR; 4.
DR PROSITE; PS00420; SRCR 1; 1.
DR PROSITE; PS50287; SRCR 2; 4.
FT NON_TER 1 1
SQ SEQUENCE 819 AA; 91379 MW; 47B9215FA842B119 CRC64;

Query Match 11.3%; Score 80; DB 13; Length 819;
Best Local Similarity 23.7%; Pred. No. 54;
Matches 28; Conservative 14; Mismatches 42; Indels 34; Gaps 2;

QY 44 LAGMCHRVLPGTGASAI-----AATVTPKGASMKLPPRPOSTK-----83
DB 49 LGVICSPPRRPGSPAVAVEEAPSSSRHQPNQPGQRPPLPQSVPPPAHSSSSARGHEI 108
QY 84 -----SPELRSLRKIREMNTISQESARVNHRLPEGHPLLEKRAYFR 127
DB 109 ALHRNPTSSRRSIISQENGHEIQILRRNRGSSRASQVNPALPQGHQLLSRLANGYR 166

RESULT 31
Q9W6N1 PRELIMINARY; PRT; 895 AA.
AC Q9W6N1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Lysyl oxidase related protein homolog.
GN FLO2.
OS Perca flavescens (Yellow perch).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Percidae; Perca.
OX NCBI_TaxID=8167;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX Langenau D.M., Goetz F.W., Roberts S.B.;
RA "The upregulation of messenger ribonucleic acids during 17alpha,
RT 20beta-dihydroxy-4-pregnen-3-one-induced ovulation in the perch
RT ovary";
RL J. Mol. Endocrinol. 23:137-152(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Roberts S.B., Goetz F.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF143003; AAD33900.1; -
DR InterPro; IPR001695; Lysyl oxidase.
DR InterPro; IPR001190; Srcr receptor.
DR Pfam; PF01186; Lysyl oxidase; 1.
DR Pfam; PF00530; SRCR; 4.
DR PRINTS; PR00074; LYSYLOXIDASE.
DR ProDom; PD013887; Lysyl oxidase; 1.
DR SMART; SM00202; SR; 4.
DR PROSITE; PS00420; SRCR 1; 1.
DR PROSITE; PS50287; SRCR 2; 4.
SQ SEQUENCE 895 AA; 99621 MW; E18627D1604896B7 CRC64;

Query Match 11.3%; Score 80; DB 13; Length 895;
Best Local Similarity 23.7%; Pred. No. 50;
Matches 28; Conservative 14; Mismatches 42; Indels 34; Gaps 2;

QY 44 LAGMCHRVLPGTGASAI-----AATVTPKGASMKLPPRPOSTK-----83
DB 125 LGVICSPPRRPGSPAVAVEEAPSSSRHQPNQPGQRPPLPQSVPPPAHSSSSARGHEI 184
QY 84 -----SPELRSLRKIREMNTISQESARVNHRLPEGHPLLEKRAYFR 127
DB 185 ALHRNPTSSRRSIISQENGHEIQILRRNRGSSRASQVNPALPQGHQLLSRLANGYR 242

RESULT 32
O81209 PRELIMINARY; PRT; 902 AA.
AC O81209;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Respiratory burst oxidase protein A.
GN RBOHA.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lardeberg erecta;
RX MEDLINE=98291500; PubMed=9628030;
RA Torres M.A., Onouchi H., Hamada S., Machida C.h., Hammond-Kosack K.E.,
RA Jones J.D.G.;
RT "Six Arabidopsis thaliana homologues of the human respiratory burst
RT oxidase (gp91phox).";
RL Plant J. 14:365-370(1998).
DR EMBL; AF055353; AAC39475.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002916; Ferric reduct.
DR InterPro; IPR000778; GP91PHOX.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01794; Ferric reduct; 1.
DR PRINTS; PR00466; GP91PHOX.
DR PROSITE; PS00018; EF HAND; 1.
SQ SEQUENCE 902 AA; 102996 MW; 02B988A97DEFB318 CRC64;

Query Match 11.3%; Score 80; DB 10; Length 902;

Best Local Similarity 25.2%; Pred. No. 60;
Matches 37; Conservative 22; Mismatches 42; Indels 46; Gaps 7;
QY 3 STSTTNFVAENRPTGTFDVFV-----MREALRV-KSERLA 39
Db 31 NVATTSNYGDEPYVEITLDIHDDSVVGLKSPNHRGAGSNYEDQSLLRQGRSRSNS 90
QY 40 MLRALAGMCHRVLPGTGASAIATVTPKGSMKLPKPPRQSTK---SPELRELSRK-IR 95
Db 91 VLKELASSV-----STGITRVASSVSSSSAR---KPPRPQLAKLRRSKRAELALKGLK 141
QY 96 EMNKTTISQESARVNHRLPEGHPLLEKR 122
Db 142 FITKTDG-----VTGWPEVEKR 158
RESULT 33
Q9LY21 PRELIMINARY; PRT; 902 AA.
AC Q9LY21
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Respiratory burst oxidase protein A.
GN T211.100.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Rudd S., Lencke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL163912; CAB87928.1; -.
DR InterPro; IPR002048; EP-hand.
DR InterPro; IPR002916; Ferric_reduct.
DR InterPro; IPR000778; GP91Phox.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01794; Ferric_reduct; 1.
DR PRINTS; PR00466; GP91PHOX.
DR PROSITE; PS00018; EF HAND; 1.
SQ SEQUENCE 902 AA; 102935 MW; E43286CAD4F857B2 CRC64;
Query Match 11.3%; Score 80; DB 10; Length 902;
Best Local Similarity 25.2%; Pred. No. 60;
Matches 37; Conservative 22; Mismatches 42; Indels 46; Gaps 7;
QY 3 STSTTNFVAENRPTGTFDVFV-----MREALRV-KSERLA 39
Db 31 NVATTSNYGDEPYVEITLDIHDDSVVGLKSPNHRGAGSNYEDQSLLRQGRSRSNS 90
QY 40 MLRALAGMCHRVLPGTGASAIATVTPKGSMKLPKPPRQSTK---SPELRELSRK-IR 95
Db 91 VLKELASSV-----STGITRVASSVSSSSAR---KPPRPQLAKLRRSKRAELALKGLK 141
QY 96 EMNKTTISQESARVNHRLPEGHPLLEKR 122
Db 142 FITKTDG-----VTGWPEVEKR 158
RESULT 34
Q8VM43 PRELIMINARY; PRT; 1017 AA.
ID Q8VM43
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Proline dehydrogenase.
GN PUTA.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GX201;
RA Wu B., Tang X., Bai X., Tang D., Lu A., Tang J., Ma O.;
RT "Bradyrhizobium japonicum strain GX201 proline dehydrogenase gene
submited (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL; AF306633; AAL35755.1; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR002872; Pro dh.
DR InterPro; IPR001580; WD40.
DR Pfam; PF00171; aldehyd; 1.
DR Pfam; PF01619; Pro dh; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
KW Oxidoreductase.
SQ SEQUENCE 1017 AA; 111472 MW; E4B350B0B4EAS5B CRC64;
Query Match 11.3%; Score 80; DB 2; Length 1017;
Best Local Similarity 18.8%; Pred. No. 70;
Matches 38; Conservative 28; Mismatches 50; Indels 86; Gaps 7;
QY 5 STTNFVAENRPTGTFDVMREALLRVKSSERLAMLRLAGMC-----GHRV 52
Db 585 SRSAHFIALLOPEGGKTLD-----DALSDLREADFRCYVAAQGRKLPASETA 632
QY 53 LPGTGASAIATVTPKGSMKLP-----PRQS----- 81
Db 633 MFGNGESNALTMRGGAFAVISPWNFFLAFLGQVTAALMAGNSVWAKPAEQTPRIARG 692
QY 82 -----TKSPELRELSRKIREMNKTTISQESARVN-----HRLPEGHPLLEKRAEYFRHLRS 131
D., 693 RSPAARSRHQPQERASRRHRPHRRRADRSRRRRRLRLDRGRP-----QHQT 743
QY 132 LKSO-----GVNRLI 141
Db 744 LAADGPIVPLIAETGGINAMI 765
RESULT 35
Q9Y069 PRELIMINARY; PRT; 211 AA.
AC Q9Y069
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative transcription factor.
GN PA-EN2.A.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=21110537; PubMed=11180849;
RA Marie B., Bacon J.P.;
RT "Two engrailed-related genes in the cockroach: cloning, phylogenetic
analysis, expression and isolation of spliced variants.";
RL Dev. Genes Evol. 210:436-448(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=20180522; PubMed=10712910;
RA Marie B., Bacon J.P., Blagburn J.M.;

"Double-stranded RNA interference shows that Engrailed controls the synaptic specificity of identified sensory neurons.";
 Curr. Biol. 10:289-292(2000).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AJ243885; CAB51043.1; -.
 DR HSSP; P02836; 3HDD.
 DR InterPro; IPR000747; Engrailed.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_lambrepresr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00026; ENGRAILED.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00033; ENGRAILED; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 211 AA; 23686 MW; 5886AB9B66885F2 CRC64;

Query Match 11.2%; Score 79.5; DB 5; Length 211;
 Best Local Similarity 29.4%; Pred. No. 12;
 Matches 32; Conservative 14; Mismatches 42; Indels 21; Gaps 5;

QY 43 ALAGMCHRVLPOTGASATAAATVTPKGSMKLP-----PRQSTKSPPELRELGRK 93
 Db 51 AIAGSPSSAV-PGASGSASSGS-----GSSQLLPAWVYCTRYSDRPSGRSPSRMRKRK 105
 QY 94 IREMNKT-----ISOESARVNHLPPEHPLLE-KRAEYFRHLRLSKSQ 135
 Db 106 DKPEKRPRTAFSGQLARLKHTEFTENRYLERRTELARELGINKAQ 154

RESULT 36
 ID Q8VYQ4 PRELIMINARY; PRT; 348 AA.
 AC Q8VYQ4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Atig24265/Atig24265).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
 RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY070135; AAL47485.1; -.
 DR EMBL; AY103301; AAM65353.1; -.
 DR InterPro; IPR000169; SHprot_acsite.

DR InterPro; IPR005829; Sug transporter.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 348 AA; 37188 MW; 26F280470E4B8B2F CRC64;

Query Match 11.2%; Score 79.5; DB 10; Length 348;
 Best Local Similarity 17.3%; Pred. No. 21;
 Matches 22; Conservative 34; Mismatches 46; Indels 25; Gaps 4;

QY 8 TNFVAENRPTGETFDVYREALLRVKSERLAM--LRALAGMC-----GHRVLPOTG 57
 Db 184 TSFIKDDVKAQVDAFENLASKVKVRIEGNQDITLGVGALHAQCCENQRIQESNKAIPST 243
 QY 58 A--SAIAATVTPKGSMKLPKPPRPOSTKSPPELRELGRK-----IREMNKTIS 102
 Db 244 SLPALEAPMAPSSKTLUSLPASPDESQSPSTPNVAOKSRGLLOHTOSMGLKIDNESS 303
 QY 103 QESARVN 109
 Db 304 SHNTSSN 310

RESULT 37
 ID Q9RKL6 PRELIMINARY; PRT; 357 AA.
 AC Q9RKL6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SCO4066.
 GN SCO4066 OR SCD25.02.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=AS3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939118; CAB56346.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 357 AA; 39169 MW; 47249F754CAGF8A3 CRC64;

Query Match 11.2%; Score 79.5; DB 16; Length 357;
 Best Local Similarity 33.3%; Pred. No. 22;
 Matches 28; Conservative 10; Mismatches 29; Indels 17; Gaps 4;

QY 10 FVAENRP-----TFGETFDVYREALLRVKSERLAMLRALAGMCHRVLPOTGASATA 62
 Db 271 FVSDGPRVRLGDLQSTGGFTLPHARQALSRPDANH-----CGTC--RLRRAGLSAVG 321
 QY 63 ATVTVPKGSMKLPKPP-RPQSTKSP 85
 Db 322 AGPSTGASRKLRLPKLPQSTPKGP 345

RESULT 38
 ID Q9P4Z1 PRELIMINARY; PRT; 4065 AA.
 AC Q9P4Z1;

01-OCT-2000 (TREMELrel. 15, Created)
 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 Related to TOM1 protein.
 BL1B22.010.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.,
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL356834; CAS92704.2; -;
 DR InterPro: IPR000569; HECT_domain.
 DR Pfam: PF00632; HECT; 1.
 DR SMART: SM00119; HECT; 1.
 DR PROSITE: PS0237; HECT; 1.
 SQ SEQUENCE 4065 AA; 452568 MW; F74683CEC36F9350 CRC64;
 Query Match 11.2%; Score 79.5; DB 3; Length 4065;
 Best Local Similarity 20.9%; Pred. No. 4.2e+02;
 Matches 34; Conservative 26; Mismatches 50; Indels 53; Gaps 7;
 QY 16 PTFGETDVMREALLRVKSSER-----LAMLALAGCMGHRVLPGTOGASIAATVTP 67
 DB 3570 PTFGKMDKLSACLSAIRQRDMNLNATILILPLIESLMVCKNTL--SDASAVSNANSQ 3627
 QY 68 KGASMKLKPRPOS-----TKSPPELSR 92
 DB 3628 K--EMLTSPPEPDRIAGLFTFTEEHRLNELVRHNPKLMGTSFSLLVKNPKVLEFDN 3685
 QY 93 KIREMNTKISQESARVNHRLPEGL-LEKRAEYFRH--LRSL 132
 DB 3686 KKNYFNRSVHSKYQTRHSF---PLQVRRVHFVHDSFSL 3725
 RESULT 39
 QYQY41 ID QY41 PRELIMINARY; PRT; 192 AA.
 AC QY41;
 DT 01-MAY-1999 (TREMELrel. 10, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Vif protein (Viron infectivity factor) (SOR protein).
 GN VIF.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fang G., Weiser B., Chappey C., Visosky A., Townsend L., Wang Q.,
 RA Burger H.,
 RT "Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to
 RT Non-Progressive Infection."
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
 DR EMBL: U69589; AAD10913.1; -;
 DR InterPro: IPR000475; Viral_infect.
 DR Pfam: PF00559; Vif; 1.
 DR PRINTS: PR00349; VIRIONINFECT.
 DR PRODOM: PD000063; Viral_infect; 1.
 KW AIDS.
 SQ SEQUENCE 192 AA; 22434 MW; BB383D104E5A7A3E CRC64;
 Query Match 11.2%; Score 79; DB 15; Length 192;
 Best Local Similarity 29.0%; Pred. No. 11;
 Matches 31; Conservative 10; Mismatches 28; Indels 38; Gaps 6;
 01-DEC-2000 (TREMELrel. 15, Created)
 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 Related to TOM1 protein.
 BL1B22.010.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.,
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL356834; CAS92704.2; -;
 DR InterPro: IPR000569; HECT_domain.
 DR Pfam: PF00632; HECT; 1.
 DR SMART: SM00119; HECT; 1.
 DR PROSITE: PS0237; HECT; 1.
 SQ SEQUENCE 4065 AA; 452568 MW; F74683CEC36F9350 CRC64;
 Query Match 11.2%; Score 79.5; DB 3; Length 4065;
 Best Local Similarity 20.9%; Pred. No. 4.2e+02;
 Matches 34; Conservative 26; Mismatches 50; Indels 53; Gaps 7;
 QY 16 PTFGETDVMREALLRVKSSER-----LAMLALAGCMGHRVLPGTOGASIAATVTP 67
 DB 3570 PTFGKMDKLSACLSAIRQRDMNLNATILILPLIESLMVCKNTL--SDASAVSNANSQ 3627
 QY 68 KGASMKLKPRPOS-----TKSPPELSR 92
 DB 3628 K--EMLTSPPEPDRIAGLFTFTEEHRLNELVRHNPKLMGTSFSLLVKNPKVLEFDN 3685
 QY 93 KIREMNTKISQESARVNHRLPEGL-LEKRAEYFRH--LRSL 132
 DB 3686 KKNYFNRSVHSKYQTRHSF---PLQVRRVHFVHDSFSL 3725

QY 22 FDMREALLRVKSSERLAMLALAGCMGHRVLPG-----TGA-----SAIAATVTPKG 69
 DB 112 FDCFSASAIR-----NAILGHRVSPSCYQAGHNKVGSLQVLAALAITPK- 157
 QY 70 ASMKLKPRPQSTKSPPELSRKIREMNTKISQESARVNHRLPEGH 116
 DB 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGRGSHTM-NGH 192
 RESULT 40
 Q73093 ID Q73093 PRELIMINARY; PRT; 192 AA.
 AC Q73093;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
 DE Vif (viral infectivity factor) (Viron infectivity factor) (SOR protein).
 GN VIF.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94303241; PubMed=8030283;
 RA Wieland U., Hartmann J., Suhr H., Salzberger B., Eggers HJ.,
 RA Kuehn J.E.;
 RT "In vivo genetic variability of the HIV-1 vif gene."
 RL Virology 203:43-51(1994).
 CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
 DR EMBL: Z30605; CA83082.1; -;
 DR InterPro: IPR000475; Viral_infect.
 DR Pfam: PF00559; Vif; 1.
 DR PRINTS: PR00349; VIRIONINFECT.
 DR PRODOM: PD000063; Viral_infect; 1.
 KW AIDS.
 SQ SEQUENCE 192 AA; 22317 MW; 2A48EFA33334900E CRC64;
 Query Match 11.2%; Score 79; DB 15; Length 192;
 Best Local Similarity 29.0%; Pred. No. 11;
 Matches 31; Conservative 10; Mismatches 28; Indels 38; Gaps 6;
 QY 22 FDMREALLRVKSSERLAMLALAGCMGHRVLPG-----TGA-----SAIAATVTPKG 69
 DB 112 FDCFSASAIR-----NAILGHRVSPSCYQAGHNKVGSLQVLAALAITPK- 157
 QY 70 ASMKLKPRPQSTKSPPELSRKIREMNTKISQESARVNHRLPEGH 116
 DB 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGRGSHTM-NGH 192
 Search completed: November 14, 2003, 10:41:39
 Job time : 71 secs

2M protein - protein search, using sw model

Run on: November 14, 2003, 10:42:41 ; Search time 41 Seconds
(without alignments)
545.865 Million cell updates/sec

Title: US-10-087-573-2
Perfect score: 141
Sequence: 1 MESTSTTNFVAENRPTFGE.....RAEYFRHLRLSKQGVNRLI 141

Scoring table: OJGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

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22: /SIDSI1/gcgdata/geneseq/geneseq-embl/AA2001.DAT:*
23: /SIDSI1/gcgdata/geneseq/geneseq-embl/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	141	100.0	141 23	ABP33714
2	126	89.4	285 23	ABP33715
3	7	5.0	16 24	ABP2389
4	7	5.0	88 22	AAU46323
5	7	5.0	97 22	AAU46323
6	7	5.0	103 22	AAU46323
7	7	5.0	141 22	AAO10778
8	7	5.0	157 22	ABP1776
9	7	5.0	159 22	ABP66671
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Propionibacterium
Drosophila melanog
Cryptosporidium sp
Novel human diagno
Human novel protei
Human protein SEQ
Human protein SEQ
Human polypeptide
Melanocortin recep
Melanocortin recep
Human melanocortin
RPP5-like protein
Melanocortin-4 rec
Melanocortin-4 rec
Human melanocortin
Homo sapiens mutan
Homo sapiens mutan
Homo sapiens mutan
Human melanocortin
Sulfolobus solfata
Human melanocortin
Human MC4 protein.
A human melanocort
Human G protein co
Human G protein co
Rhesus monkey mela
Synthetic labeled
Melanocortin-4 rec
Amino acid sequenc
Human melanocortin
Human melanocortin
Melanocortin recep
Melanocortin recep
Human melanocortin
Human melanocortin
Pseudomonas aerugi
Listeria monocytog
Chlamydomonas inte
Drosophila melanog
Mycobacterium tube
Glycine max oil tr
Aspergillus thalia
Aspergillus fumiga
E. coli cellular p
Arabidopsis thalia
Arabidopsis thalia
Aspergillus fumiga
Novel human diagno
Drosophila melanog
Drosophila melanog
Subsequence which
Peptidomimetic of
Human C35 peptide
Human 34P3D7 HLA A
Human 34P3D7 HLA A
Tropoin 1 peptide
Peptidomimetic of
Human HES 2 transc
Calmodulin inhibit
Human T lymphocyte
Polypeptide fragme
Human secreted pro
Human apo-lipoprot
Peptide #5053 enco
Peptide #5186 enco
Human AGE receptor
Human tropoelastin
Human tropoelastin
Human liver peptid
Peptide #1585 enco
Peptide #1611 enco
Protein #1542 enco
Human brain expres

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11 203 22 ABB67442
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13 214 22 ABB67442
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83	6	4.3	34	22	AAM67272	Human bone marrow	156	6	4.3	73	22	AAU49005	Propionibacterium
84	6	4.3	34	22	AAM15111	Peptide #1545 enco	157	6	4.3	75	24	ABJ26268	Aspergillus fumiga
85	6	4.3	34	22	AAM77566	Peptide #1503 enco	158	6	4.3	76	20	AAV16642	WO9914235 Seg ID N
86	6	4.3	34	22	AAM02852	Peptide #1534 enco	159	6	4.3	76	22	AAU62764	Propionibacterium
87	6	4.3	34	23	ABG36921	Human peptide enco	160	6	4.3	77	21	AAU14470	Arabidopsis thalia
88	6	4.3	40	18	AAW20291	H. pylori cell env	161	6	4.3	77	22	ABG19038	Novel human diagno
89	6	4.3	40	21	AAW25024	Plant SDF encoded	162	6	4.3	77	23	ABBB8163	C bullatus mu-coco
90	6	4.3	41	15	AAAG60064	Antimicrobial pept	163	6	4.3	78	22	AAO00583	Human polypeptide
91	6	4.3	41	16	AAAR80734	Synthetic antimicr	164	6	4.3	78	23	ABP32744	Human ORFX protein
92	6	4.3	43	21	AAK25022	Plant SDF encoded	165	6	4.3	78	23	ABP01837	Human ORFX protein
93	6	4.3	44	21	AAK55117	Arabidopsis thalia	166	6	4.3	78	23	ABBB8165	C bullatus mu-coco
94	6	4.3	45	22	ABG54790	Human liver peptid	167	6	4.3	79	20	AAV19550	Amino acid sequenc
95	6	4.3	45	22	AAW73075	Human bone marrow	168	6	4.3	80	22	ABG13188	Novel human diagno
96	6	4.3	45	22	AAAB85442	Human immune/haema	169	6	4.3	80	22	AAAG1600	Human immune/haema
97	6	4.3	45	22	AAAM33294	Peptide #7331 enco	170	6	4.3	81	21	AAAG14469	Arabidopsis thalia
98	6	4.3	45	23	ABG42920	Human peptide enco	171	6	4.3	82	21	AAAG08450	Arabidopsis thalia
99	6	4.3	51	23	ABG58273	Human liver peptid	172	6	4.3	82	23	ABP31546	Human ORF519 prote
100	6	4.3	51	22	ABBA42867	Peptide #10373 enco	173	6	4.3	83	21	AAV79172	P. carinii major s
101	6	4.3	51	22	ABBB6139	Protein #8138 enco	174	6	4.3	83	22	AAU65887	Propionibacterium
102	6	4.3	51	22	AAAG3760	Human brain expres	175	6	4.3	84	22	AAU45110	Propionibacterium
103	6	4.3	51	22	AAAG76574	Human bone marrow	176	6	4.3	84	22	AAU65766	Propionibacterium
104	6	4.3	51	22	AAAM36681	Peptide #10718 enco	177	6	4.3	86	21	AAAB53242	Human colon cancer
105	6	4.3	51	23	ABG45822	Human peptide enco	178	6	4.3	86	22	AAU56609	Propionibacterium
106	6	4.3	51	23	ABP09059	Human ORFX protein	179	6	4.3	87	22	ABBB11339	Human beta-fibrino
107	6	4.3	52	22	ABG55673	Human liver peptid	180	6	4.3	88	22	AAAM25265	Human protein sequ
108	6	4.3	52	22	ABBA40394	Peptide #7900 enco	181	6	4.3	89	23	ABG65221	Human albumin fusi
109	6	4.3	52	22	ABBA24766	Protein #6765 enco	182	6	4.3	89	23	ABP02302	Human ORFX protein
110	6	4.3	52	22	AAAM61202	Human brain expres	183	6	4.3	89	23	AAU91086	Human secreted pro
111	6	4.3	52	22	AAAM73921	Human bone marrow	184	6	4.3	90	22	AAU43952	Propionibacterium
112	6	4.3	52	22	AAAM20157	Peptide #6591 enco	185	6	4.3	90	22	AAU57366	Propionibacterium
113	6	4.3	52	22	AAAM34100	Peptide #8137 enco	186	6	4.3	90	22	AAAB31654	Amino acid sequenc
114	6	4.3	52	23	ABG43809	Human peptide enco	187	6	4.3	95	20	AAV16644	WO9914235 Seg ID N
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116	6	4.3	53	20	AAW89089	Polypeptide fragme	189	6	4.3	97	22	AAU65570	Propionibacterium
117	6	4.3	55	21	AAAG55116	Arabidopsis thalia	190	6	4.3	97	22	AG91239	C glutamic prote
118	6	4.3	55	22	ABG48446	Human liver peptid	191	6	4.3	101	23	ABR01707	Human breast speci
119	6	4.3	55	22	ABBB28423	Peptide #1074 enco	192	6	4.3	104	21	AAAB41199	Human ORFX ORF963
120	6	4.3	55	22	ABBB33604	Peptide #1110 enco	193	6	4.3	106	21	AAAG18180	Arabidopsis thalia
121	6	4.3	55	22	ABBS1262	Human secreted pro	194	6	4.3	106	21	AAAG32862	Zea mays protein f
122	6	4.3	55	22	ABBB19059	Protein #1058 enco	195	6	4.3	106	21	AAAG45788	Arabidopsis thalia
123	6	4.3	55	22	ABBB02328	Human musculoskele	196	6	4.3	107	19	AAW75892	Peptide inhibitor
124	6	4.3	55	22	AAW54377	Human brain expres	197	6	4.3	107	19	AAW75895	Peptide inhibitor
125	6	4.3	55	22	AAAM66778	Human bone marrow	198	6	4.3	107	21	AAW78860	Streptomycin subti
126	6	4.3	55	22	AAAM14644	Peptide #1078 enco	199	6	4.3	107	23	ABP09234	Human ORFX protein
127	6	4.3	55	22	AAAM27063	Peptide #1051 enco	200	6	4.3	110	21	AAAG54411	Zea mays protein f
128	6	4.3	55	23	ABP52814	Medane and bHLH do	201	6	4.3	111	15	AAAG60099	Human secreted pro
129	6	4.3	55	23	ABG36433	Human peptide enco	202	6	4.3	111	15	AAAG60099	Antimicrobial prot
130	6	4.3	55	24	ABU12532	Novel human muscul	203	6	4.3	111	23	ABP09265	Human ORFX protein
131	6	4.3	56	22	AAW87268	Human immune/haema	204	6	4.3	113	22	AAU39573	Propionibacterium
132	6	4.3	58	21	AAAG09191	Arabidopsis thalia	205	6	4.3	114	22	AAU65156	Propionibacterium
133	6	4.3	58	22	AAU58303	Propionibacterium	206	6	4.3	118	21	AAAG00151	Human secreted pro
134	6	4.3	58	22	AAW89013	Human immune/haema	207	6	4.3	118	22	AAO01462	Human polypeptide
135	6	4.3	58	23	ABP52813	Medane and bHLH do	208	6	4.3	119	22	ABBB6813	Drosophila melanog
136	6	4.3	59	22	AAAG9862	ERA binding domain	209	6	4.3	120	21	AAAB58812	Breast and ovarian
137	6	4.3	60	23	ABP00702	Human ORFX protein	210	6	4.3	121	20	AAV49627	Corn hexose carrie
138	6	4.3	61	18	AAW20768	H. pylori cell env	211	6	4.3	121	21	AAAB53802	Human colon cancer
139	6	4.3	62	22	ABBB95797	Human testicular a	212	6	4.3	121	21	AAAG18179	Arabidopsis thalia
140	6	4.3	62	22	AAAG95092	Human reproductive	213	6	4.3	121	21	AAAG45787	Arabidopsis thalia
141	6	4.3	63	23	ABP38041	Staphylococcus epi	214	6	4.3	121	22	AAO01815	Human polypeptide
142	6	4.3	64	22	AAU52676	Propionibacterium	215	6	4.3	124	22	AAAG181915	S. epidermidis ope
143	6	4.3	64	22	ABG13937	Novel human diagno	216	6	4.3	125	21	AAAG18530	Zea mays protein f
144	6	4.3	68	22	ABP08983	Human ORFX protein	217	6	4.3	126	21	AAAG14595	Arabidopsis thalia
145	6	4.3	68	24	ABR41698	Human DITHP riboso	218	6	4.3	126	20	AAU04808	Mycobacterium spec
146	6	4.3	69	21	AAV71961	Rat pituitary horm	219	6	4.3	128	23	ABU05760	M. tuberculosis an
147	6	4.3	69	22	AAU42690	Propionibacterium	220	6	4.3	128	23	ABU05760	Human protein sequ
148	6	4.3	69	22	AAW80886	Human haematologic	221	6	4.3	129	23	ABP05151	Human ORFX protein
149	6	4.3	69	22	AAAM1352	Human haematologic	222	6	4.3	131	14	AAAB38222	Sequence of polype
150	6	4.3	69	22	AAAB1653	Human haematologic	223	6	4.3	131	14	AAAB38222	Human protein sequ
151	6	4.3	69	22	AAAB1653	Human haematologic	224	6	4.3	135	21	AAAB38222	Human protein sequ
152	6	4.3	70	21	AAAG08451	Arabidopsis thalia	225	6	4.3	135	21	AAAB38222	Arabidopsis thalia
153	6	4.3	70	21	AAAG08451	Arabidopsis thalia	226	6	4.3	135	22	ABBB69313	Drosophila melanog
154	6	4.3	70	23	ABBB9457	L. helveticus exop	227	6	4.3	135	23	ABP34790	Human synthase-lik
155	6	4.3	71	23	ABBB8631	Conus magus I-supe	228	6	4.3	135	23	AAE21290	Human Mrg (mas-rel

229 Human Mrg (mas-rel 4.3 135 AAE21295
230 Antigen tc-33c. E 4.3 136 AR22397
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234 Human novel extrac 4.3 143 AAU19656
235 Human polypeptide 4.3 143 ABP47876
236 Propionibacterium 4.3 144 AAU63847
237 Lactococcus lactis 4.3 144 ABP54326
238 Drosophila melanog 4.3 145 ABP66141
239 Human secreted pro 4.3 149 AAU94985
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241 Helicobacter pylori 4.3 151 AAU51606
242 Human polypeptide 4.3 152 AAU41826
243 Consensus sodium/c 4.3 152 ABP84484
244 Arabidopsis thalia 4.3 153 AAG14594
245 Streptococcus poly 4.3 153 ABP27677
246 Streptococcus poly 4.3 153 ABP29821
247 S. pneumoniae deri 4.3 158 AAU65930
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249 S. pneumoniae type 4.3 158 AAU00803
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253 Novel human secret 4.3 161 AAU31459
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257 Staphylococcus epi 4.3 163 ABP18264
258 Human colon cancer 4.3 164 ABP75966
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264 Amino acid sequenc 4.3 171 AAU69137
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270 Human prion-like m 4.3 176 AAU82498
271 Human prion-relate 4.3 176 AAU70942
272 Human PRO3443. Ho 4.3 176 AAU87558
273 Human Dpl. Homo s 4.3 176 AAU49404
274 Human secreted/tra 4.3 176 AAU95923
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276 Human secreted pol 4.3 176 AAU71578
277 Novel human secret 4.3 176 AAU72024
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290 Human novel polype 4.3 177 AAU00340
291 Drosophila melanog 4.3 178 AAU68838
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293 Human transcriptio 4.3 179 AAU50219
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295 Human protein HP10 4.3 179 AAG33274
296 Mouse prion-like m 4.3 179 AAB82499
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Drosophila melanog
Human polypeptide
Human oxidoreducta
Bacillus cereus ve
H. pylori GHPO 160
Arabidopsis thalia
Arabidopsis thalia
Pseudomonas aerugi
Pseudomonas aerugi
Erysipelas protect
Arabidopsis thalia
Human polypeptide
Candida albicans e
Propionibacterium
C glutamicum prote
Drosophila melanog
Drosophila melanog
Human novel secret
Human novel polype
Arabidopsis thalia
Staphylococcus epi
Staphylococcus epi
Protein involved i
Mouse pre-pro-neur
WO9914235 Seq ID N
Arabidopsis thalia
Drosophila melanog
Human tropoelastin
Human novel secret
Human novel polype
C glutamicum prote
Chlamydia pneumonia
Chlamydia pneumonia
Arabidopsis thalia
Arabidopsis thalia
Staphylococcus aur
Staphylococcus aur
Staphylococcus aur
Arabidopsis thalia
Polypeptide-riboso
Human polypeptide
Human ORFX ORF2933
Novel human secret
Human tropoelastin
Novel human DNA-B1
Human DNA-binding
Human ovarian anti
Amino acid sequenc
Propionibacterium
Human polypeptide
Novel secreted pro
Propionibacterium
I. scapularis Salp
Human protein HP00
Human polypeptide
Chlamydia pneumonia
C. pneumoniae CPN1
Lactococcus lactis
Novel human diagno
DPP10 homologous p
Arabidopsis thalia
Propionibacterium
C glutamicum prote
Corynebacterium gl
Mycobacterium spec
Arabidopsis thalia
Helicobacter pylori
Sequence #1 homolo
S. epidermidis ope
Staphylococcus epi
Enterococcus faeca
E faecalis EF040 a

375	238	23	ABP09432	Human ORFX protein	448	6	4.3	251	23	ABP44007	Human Blys binding
376	238	24	ABU13585	Enterococcus faeca	449	6	4.3	251	23	ABP44008	Human Blys binding
377	239	21	AAG4692	Zea mays protein f	450	6	4.3	251	23	ABP44009	Human Blys binding
378	239	22	AAG45311	Arabidopsis thalia	451	6	4.3	251	23	ABP44010	Human Blys binding
379	239	22	AAU18322	Human endocrine po	452	6	4.3	251	23	ABP44011	Human Blys binding
380	242	23	ABG65136	Human albumin fusi	453	6	4.3	251	23	ABP44012	Human Blys binding
381	242	23	ABP45819	Human Blys binding	454	6	4.3	251	23	ABP44013	Human Blys binding
382	242	23	ABP45833	Human Blys binding	455	6	4.3	251	23	ABP44014	Human Blys binding
383	242	23	ABP45803	Human secreted pro	456	6	4.3	251	23	ABP44015	Human Blys binding
384	243	23	ABP45504	Human Blys binding	457	6	4.3	251	23	ABP44016	Human Blys binding
385	243	23	ABP45522	Human Blys binding	458	6	4.3	251	23	ABP44017	Human Blys binding
386	243	23	ABP45582	Human Blys binding	459	6	4.3	251	23	ABP44018	Human Blys binding
387	244	23	ABP45113	Human Blys binding	460	6	4.3	251	23	ABP44019	Human Blys binding
388	244	23	ABP45480	Human Blys binding	461	6	4.3	251	23	ABP44020	Human Blys binding
389	244	23	ABP45487	Human Blys binding	462	6	4.3	251	23	ABP44021	Human Blys binding
390	244	23	ABP45513	Human Blys binding	463	6	4.3	251	23	ABP44022	Human Blys binding
391	244	23	ABP45557	Human Blys binding	464	6	4.3	251	23	ABP44023	Human Blys binding
392	244	23	ABP45558	Human Blys binding	465	6	4.3	251	23	ABP44024	Human Blys binding
393	244	23	ABP45571	Human Blys binding	466	6	4.3	251	23	ABP44025	Human Blys binding
394	244	23	ABP45834	Human Blys binding	467	6	4.3	251	23	ABP44026	Human Blys binding
395	245	23	ABP45505	Human Blys binding	468	6	4.3	251	23	ABP44027	Human Blys binding
396	245	23	ABP45510	Human Blys binding	469	6	4.3	251	23	ABP44028	Human Blys binding
397	245	23	ABP45512	Human Blys binding	470	6	4.3	251	23	ABP44029	Human Blys binding
398	245	23	ABP45517	Human Blys binding	471	6	4.3	251	23	ABP44030	Human Blys binding
399	245	23	ABP45521	Human Blys binding	472	6	4.3	251	23	ABP44031	Human Blys binding
400	245	23	ABP45536	Human Blys binding	473	6	4.3	251	23	ABP44032	Human Blys binding
401	245	23	ABP45539	Human Blys binding	474	6	4.3	251	23	ABP44033	Human Blys binding
402	245	23	ABP45828	Human Blys binding	475	6	4.3	251	23	ABP44034	Human Blys binding
403	245	23	ABP45835	Human Blys binding	476	6	4.3	251	23	ABP44035	Human Blys binding
404	246	23	ABP45849	Human Blys binding	477	6	4.3	251	23	ABP44036	Human Blys binding
405	246	23	ABP45823	Human Blys binding	478	6	4.3	251	23	ABP44044	Human Blys binding
406	247	22	AAU01661	Human secreted pro	479	6	4.3	251	23	ABP44050	Human Blys binding
407	247	23	ABP45481	Human Blys binding	480	6	4.3	251	23	ABP44053	Human Blys binding
408	247	23	ABP45700	Human Blys binding	481	6	4.3	251	23	ABP44054	Human Blys binding
409	248	21	AAU78932	Porcine melanocort	482	6	4.3	251	23	ABP44056	Human Blys binding
410	248	22	ABU08751	Porcine melanocort	483	6	4.3	251	23	ABP44057	Human Blys binding
411	248	22	ABP44100	Human Blys binding	484	6	4.3	251	23	ABP44059	Human Blys binding
412	250	23	ABP44037	Human Blys binding	485	6	4.3	251	23	ABP44060	Human Blys binding
413	250	23	ABP44038	Human Blys binding	486	6	4.3	251	23	ABP44061	Human Blys binding
414	250	23	ABP44039	Human Blys binding	487	6	4.3	251	23	ABP44068	Human Blys binding
415	250	23	ABP44040	Human Blys binding	488	6	4.3	251	23	ABP44072	Human Blys binding
416	250	23	ABP44041	Human Blys binding	489	6	4.3	251	23	ABP44073	Human Blys binding
417	250	23	ABP44042	Human Blys binding	490	6	4.3	251	23	ABP44074	Human Blys binding
418	250	23	ABP44043	Human Blys binding	491	6	4.3	251	23	ABP44075	Human Blys binding
419	250	23	ABP44045	Human Blys binding	492	6	4.3	251	23	ABP44076	Human Blys binding
420	250	23	ABP44046	Human Blys binding	493	6	4.3	251	23	ABP44077	Human Blys binding
421	250	23	ABP44047	Human Blys binding	494	6	4.3	251	23	ABP44078	Human Blys binding
422	250	23	ABP44048	Human Blys binding	495	6	4.3	251	23	ABP44079	Human Blys binding
423	250	23	ABP44049	Human Blys binding	496	6	4.3	251	23	ABP44080	Human Blys binding
424	250	23	ABP44051	Human Blys binding	497	6	4.3	251	23	ABP44081	Human Blys binding
425	250	23	ABP44052	Human Blys binding	498	6	4.3	251	23	ABP44082	Human Blys binding
426	250	23	ABP44055	Human Blys binding	499	6	4.3	251	23	ABP44083	Human Blys binding
427	250	23	ABP44058	Human Blys binding	500	6	4.3	251	23	ABP44084	Human Blys binding
428	250	23	ABP44062	Human Blys binding	501	6	4.3	251	23	ABP44085	Human Blys binding
429	250	23	ABP44063	Human Blys binding	502	6	4.3	251	23	ABP44086	Human Blys binding
430	250	23	ABP44064	Human Blys binding	503	6	4.3	251	23	ABP44087	Human Blys binding
431	250	23	ABP44065	Human Blys binding	504	6	4.3	251	23	ABP44088	Human Blys binding
432	250	23	ABP44066	Human Blys binding	505	6	4.3	251	23	ABP44090	Human Blys binding
433	250	23	ABP44067	Human Blys binding	506	6	4.3	251	23	ABP44091	Human Blys binding
434	250	23	ABP44069	Human Blys binding	507	6	4.3	251	23	ABP44092	Human Blys binding
435	250	23	ABP44070	Human Blys binding	508	6	4.3	251	23	ABP44093	Human Blys binding
436	250	23	ABP44089	Human Blys binding	509	6	4.3	251	23	ABP44095	Human Blys binding
437	250	23	ABP44096	Human Blys binding	510	6	4.3	251	23	ABP44097	Human Blys binding
438	250	23	ABP44129	Human Blys binding	511	6	4.3	251	23	ABP44098	Human Blys binding
439	251	23	ABP43998	Human Blys binding	512	6	4.3	251	23	ABP44099	Human Blys binding
440	251	23	ABP43999	Human Blys binding	513	6	4.3	251	23	ABP44101	Human Blys binding
441	251	23	ABP44000	Human Blys binding	514	6	4.3	251	23	ABP44102	Human Blys binding
442	251	23	ABP44001	Human Blys binding	515	6	4.3	251	23	ABP44103	Human Blys binding
443	251	23	ABP44002	Human Blys binding	516	6	4.3	251	23	ABP44104	Human Blys binding
444	251	23	ABP44003	Human Blys binding	517	6	4.3	251	23	ABP44105	Human Blys binding
445	251	23	ABP44004	Human Blys binding	518	6	4.3	251	23	ABP44106	Human Blys binding
446	251	23	ABP44005	Human Blys binding	519	6	4.3	251	23	ABP44107	Human Blys binding
447	251	23	ABP44006	Human Blys binding	520	6	4.3	251	23	ABP44108	Human Blys binding

667	6	4.3	251	23	ABP44263	Human Blys binding	740	6	4.3	260	24	ABU71569	Human secreted pol
668	6	4.3	251	23	ABP44264	Human Blys binding	741	6	4.3	260	24	ABU72015	Novel human secret
669	6	4.3	251	23	ABP44265	Human Blys binding	742	6	4.3	260	24	ABU72172	Human PRO polypept
670	6	4.3	251	23	ABP44266	Human Blys binding	743	6	4.3	260	24	ABU65757	Human secreted/tra
671	6	4.3	251	23	ABP44267	Human Blys binding	744	6	4.3	260	24	ABU66090	Novel human secret
672	6	4.3	251	23	ABP44268	Human Blys binding	745	6	4.3	260	24	ABU67594	Human secreted/tra
673	6	4.3	251	23	ABP44269	Human Blys binding	746	6	4.3	260	24	ABU65452	Human PRO polypept
674	6	4.3	251	23	ABP44270	Human Blys binding	747	6	4.3	260	24	ABU65452	Human PRO polypept
675	6	4.3	251	23	ABP44271	Human Blys binding	748	6	4.3	260	24	ABU56124	Human secreted/tra
676	6	4.3	251	23	ABP44272	Human Blys binding	749	6	4.3	260	24	ABU56722	Lung cancer-associ
677	6	4.3	251	23	ABP44273	Human Blys binding	750	6	4.3	260	24	ABU57119	Human PRO polypept
678	6	4.3	251	23	ABP44274	Human Blys binding	751	6	4.3	260	24	ABR00094	Human gene 84 enco
679	6	4.3	251	23	ABP44275	Human Blys binding	752	6	4.3	260	24	ABU10698	Human secreted/tra
680	6	4.3	251	23	ABP44276	Human Blys binding	753	6	4.3	261	22	ABG15226	Novel human diagno
681	6	4.3	251	23	ABP44277	Human Blys binding	754	6	4.3	261	22	ABP40090	Staphylococcus epi
682	6	4.3	251	23	ABP44278	Human Blys binding	755	6	4.3	262	21	AAV71962	Consensus sequenc
683	6	4.3	251	23	ABP44279	Human Blys binding	756	6	4.3	262	22	ABU10216	Human CDNA SEQ ID
684	6	4.3	251	23	ABP44280	Human Blys binding	757	6	4.3	262	22	AAU23023	Novel human enzyme
685	6	4.3	251	23	ABP44281	Human Blys binding	758	6	4.3	262	22	AAU18448	Human endocrine po
686	6	4.3	251	23	ABP44282	Human Blys binding	759	6	4.3	262	22	ABP66803	Human polypeptide
687	6	4.3	251	23	ABP44283	Human Blys binding	760	6	4.3	262	20	AAV19757	SEQ ID NO 475 from
688	6	4.3	251	23	ABP44284	Human Blys binding	761	6	4.3	264	21	AAV66637	Membrane-bound pro
689	6	4.3	251	23	ABP44285	Human Blys binding	762	6	4.3	264	21	AAV57942	Human transmembran
690	6	4.3	251	23	ABP44286	Human Blys binding	763	6	4.3	264	22	AAU29029	Human PRO polypept
691	6	4.3	251	23	ABP44287	Human Blys binding	764	6	4.3	264	22	AAU78410	Human protein SEQ
692	6	4.3	251	23	ABP44288	Human Blys binding	765	6	4.3	264	22	AAU65160	Human PRO194 (UNQ
693	6	4.3	251	23	ABP44289	Human Blys binding	766	6	4.3	264	23	ABP79335	Human ovary specif
694	6	4.3	251	23	ABP44290	Human Blys binding	767	6	4.3	264	23	ABP89985	Human polypeptide
695	6	4.3	251	23	ABP44291	Human Blys binding	768	6	4.3	264	24	ABU71117	Human PRO194 prote
696	6	4.3	251	23	ABP44292	Human Blys binding	769	6	4.3	264	24	ABU65574	Human secreted/tra
697	6	4.3	251	23	ABP44293	Human Blys binding	770	6	4.3	264	24	ABU65907	Novel human secret
698	6	4.3	251	23	ABP44294	Human Blys binding	771	6	4.3	264	24	ABU65741	Human secreted/tra
699	6	4.3	251	23	ABP44295	Human Blys binding	772	6	4.3	264	24	ABU65269	Human PRO polypept
700	6	4.3	251	23	ABP44296	Human Blys binding	773	6	4.3	264	24	ABU59053	Novel human secret
701	6	4.3	251	23	ABP44297	Human Blys binding	774	6	4.3	264	24	ABU59200	Human secreted/tra
702	6	4.3	251	23	ABP44298	Human Blys binding	775	6	4.3	264	24	ABU59349	Novel human secret
703	6	4.3	251	23	ABP44299	Human Blys binding	776	6	4.3	264	24	ABU60484	Human secreted/tra
704	6	4.3	251	23	ABP44300	Human Blys binding	777	6	4.3	264	24	ABU57975	Human PRO polypept
705	6	4.3	251	23	ABP44301	Human Blys binding	778	6	4.3	264	24	ABU58405	Human PRO polypept
706	6	4.3	251	23	ABP44302	Human Blys binding	779	6	4.3	264	24	ABU58906	Human secreted/tr
707	6	4.3	251	23	ABP44303	Human Blys binding	780	6	4.3	264	24	ABU55941	Human secreted/tra
708	6	4.3	251	23	ABP44304	Human Blys binding	781	6	4.3	264	24	ABU56936	Human PRO polypept
709	6	4.3	251	23	ABP44305	Human Blys binding	782	6	4.3	264	24	ABU13856	Human PRO194 polyp
710	6	4.3	251	23	ABP44306	Human Blys binding	783	6	4.3	264	24	ABU10515	Human secreted/tra
711	6	4.3	251	23	ABP44307	Human Blys binding	784	6	4.3	264	24	ABU10821	Human PRO polypept
712	6	4.3	251	23	ABP44308	Human Blys binding	785	6	4.3	266	21	AAU41735	Human ORFX ORF1499
713	6	4.3	251	23	ABP44309	Human Blys binding	786	6	4.3	267	20	AAU00086	Enterococcus faeca
714	6	4.3	251	23	ABP44310	Human Blys binding	787	6	4.3	267	23	ABG70509	Human ribosome S11
715	6	4.3	251	23	ABP44311	Human Blys binding	788	6	4.3	267	23	ABP43305	E faecalis EF040 p
716	6	4.3	251	23	ABP44312	Human Blys binding	789	6	4.3	267	23	ABP94074	Human secreted pro
717	6	4.3	251	23	ABP44313	Human Blys binding	790	6	4.3	267	24	ABU13584	Enterococcus faeca
718	6	4.3	251	23	ABP44314	Human Blys binding	791	6	4.3	272	21	AAU77124	Human neurotransmi
719	6	4.3	251	23	ABP44315	Human Blys binding	792	6	4.3	272	23	ABU51878	Helicobacter pylor
720	6	4.3	251	23	ABP44316	Human Blys binding	793	6	4.3	274	22	AAU05258	Dog stem cell fact
721	6	4.3	251	23	ABP44317	Human Blys binding	794	6	4.3	274	22	AAU05258	Dog SCF protein SE
722	6	4.3	251	23	ABP44318	Human Blys binding	795	6	4.3	274	22	AAU02485	Dog SCF (stem cell
723	6	4.3	251	23	ABP44319	Human Blys binding	796	6	4.3	274	22	AAU02771	Dog SCF (stem cell
724	6	4.3	251	23	ABP44320	Human Blys binding	797	6	4.3	274	22	AAU02771	Dog SCF (stem cell
725	6	4.3	251	23	ABP44321	Human Blys binding	798	6	4.3	274	22	AAU02771	Dog SCF (stem cell
726	6	4.3	251	23	ABP44322	Human Blys binding	799	6	4.3	274	22	AAU02771	Dog SCF (stem cell
727	6	4.3	251	23	ABP44323	Human Blys binding	800	6	4.3	275	23	ABP25835	Streptococcus poly
728	6	4.3	251	23	ABP44324	Human Blys binding	801	6	4.3	275	23	ABP25835	Listeria monocytog
729	6	4.3	251	23	ABP44325	Human Blys binding	802	6	4.3	276	21	ABP49384	Arabidopsis circad
730	6	4.3	251	23	ABP44326	Human Blys binding	803	6	4.3	276	22	ABP11763	Human REM2 homolog
731	6	4.3	251	23	ABP44327	Human Blys binding	804	6	4.3	276	22	AAU79740	Human protein SEQ
732	6	4.3	251	23	ABP44328	Human Blys binding	805	6	4.3	277	22	ABP11893	Human novel protei
733	6	4.3	251	23	ABP44329	Human Blys binding	806	6	4.3	277	22	ABP11893	Human protein SEQ
734	6	4.3	251	23	ABP44330	Human Blys binding	807	6	4.3	280	21	AAU19933	Arabidopsis thalia
735	6	4.3	251	23	ABP44331	Human Blys binding	808	6	4.3	280	21	AAU19933	Arabidopsis thalia
736	6	4.3	251	23	ABP44332	Human Blys binding	809	6	4.3	281	21	AAU39370	Gene 18 human secr
737	6	4.3	251	23	ABP44333	Human Blys binding	810	6	4.3	281	21	AAU39371	Human secreted pro
738	6	4.3	251	23	ABP44334	Human Blys binding	811	6	4.3	281	21	AAU19932	Arabidopsis thalia
739	6	4.3	251	23	ABP44335	Human Blys binding	812	6	4.3	281	22	AAU32365	Arabidopsis thalia
						Human PRO1774 prot						AAU32365	Putative deoxyribo

813	6	4.3	282	21	AGI19931	Arabidopsis thalia	886	6	4.3	342	20	AAW99021	Chlamydia trachoma
814	6	4.3	282	21	AGI2364	Arabidopsis thalia	887	6	4.3	343	14	AAW1670	Porcine sialyltransferase
815	6	4.3	282	21	AAU36009	Helicobacter pylori	888	6	4.3	343	16	AAW65240	Porcine ST30 sialyltransferase
816	6	4.3	282	21	AAE02488	Arabidopsis thalia	889	6	4.3	344	22	AAW90406	C glutamicum protease
817	6	4.3	282	21	AAE43822	Human cancer assoc	890	6	4.3	344	22	AAW79096	Corynebacterium gl
818	6	4.3	285	22	ABG13938	Novel human diagno	891	6	4.3	344	24	ABP78043	N. gonorrhoeae ami
819	6	4.3	285	22	ABG91376	Purine/pyrimidine	892	6	4.3	345	23	AAW15493	Beta vulgaris dihydro-oro
820	6	4.3	288	20	AAI29081	T. gondii immunogen	893	6	4.3	345	22	AAW70773	Potato dihydro-oro
821	6	4.3	288	20	AAI29082	T. gondii immunogen	894	6	4.3	346	22	AAW70779	Potato dihydro-oro
822	6	4.3	288	22	AAU25552	T. gondii immunogen	895	6	4.3	346	21	AAW23446	Arabidopsis thalia
823	6	4.3	288	22	AAU25553	T. gondii immunogen	896	6	4.3	348	21	AAW44691	Zea mays protein f
824	6	4.3	288	23	ABW54054	Lactococcus lactis	897	6	4.3	348	22	ABW68968	Drosophila melanog
825	6	4.3	289	22	ABW64653	Protein encoded by	898	6	4.3	349	8	AAW70483	Sequence of gpi en
826	6	4.3	290	20	AAI42389	Amino acid sequenc	899	6	4.3	353	21	AAW55869	Arabidopsis thalia
827	6	4.3	290	22	AAU39081	Human secreted pro	900	6	4.3	353	21	AAW61589	Arabidopsis thalia
828	6	4.3	290	23	AAO18610	Synechocystis HhoA	901	6	4.3	353	22	ABW63007	Drosophila melanog
829	6	4.3	290	23	ABW55790	Human polypeptide	902	6	4.3	357	20	AAW35069	Chlamydia pneumoni
830	6	4.3	292	24	ABU56537	Lung cancer-associ	903	6	4.3	358	21	AAW35069	Human cell surface
831	6	4.3	293	22	ABW69343	Drosophila melanog	904	6	4.3	358	20	AAW41690	Human PRO329 prote
832	6	4.3	293	22	ABG26384	Novel human diagno	905	6	4.3	359	21	AAW44246	Human secreted pro
833	6	4.3	293	23	ABW69099	Ribosyltransferase	906	6	4.3	359	21	AAW34744	Human secreted pro
834	6	4.3	294	17	AAW88003	Delta-endotoxin MK	907	6	4.3	359	21	AAW55868	Arabidopsis thalia
835	6	4.3	294	22	ABW69400	Drosophila melanog	908	6	4.3	359	21	AAW61588	Arabidopsis thalia
836	6	4.3	296	22	AAW79448	Human protein SEQ	909	6	4.3	359	22	AAU29044	Human PRO polypept
837	6	4.3	296	23	ABP43778	FLJ14840 fis clone	910	6	4.3	359	22	AAW34351	Human gene 25 enco
838	6	4.3	296	23	ABG91476	Purine/pyrimidine	911	6	4.3	359	23	AAW63386	Human albumin fusi
839	6	4.3	297	23	ABW90648	Chlamydia pneumoni	912	6	4.3	359	24	ABW47894	Human secreted pro
840	6	4.3	300	24	ABP78818	N. gonorrhoeae ami	913	6	4.3	359	24	ABU71132	Human PRO329 prote
841	6	4.3	305	21	AAW55870	Arabidopsis thalia	914	6	4.3	359	24	ABU71132	Human secreted/pro
842	6	4.3	305	21	AAW61590	Arabidopsis thalia	915	6	4.3	359	24	ABU71132	Novel human secret
843	6	4.3	306	22	ABW62221	Drosophila melanog	916	6	4.3	359	24	ABU67426	Human secreted/tr
844	6	4.3	307	22	AAW38989	Human polypeptide	917	6	4.3	359	24	ABU67426	Human PRO329 polyp
845	6	4.3	307	22	AAW38989	Human protein sequ	918	6	4.3	359	24	ABU61076	Human PRO polypept
846	6	4.3	307	22	AAW36211	Human immune syste	919	6	4.3	359	24	ABU65284	Human PRO polypept
847	6	4.3	307	23	ABP65088	Hypoxia-repressed	920	6	4.3	359	24	ABU58420	Human PRO polypept
848	6	4.3	307	23	ABW90186	Human polypeptide	921	6	4.3	359	24	ABU55956	Human secreted/tr
849	6	4.3	309	22	ABW67252	Drosophila melanog	922	6	4.3	359	24	ABU56951	Human PRO polypept
850	6	4.3	314	22	AAW80387	Secreted protein e	923	6	4.3	359	24	ABR00153	Human gene 143 enc
851	6	4.3	314	23	ABG55288	Human albumin fusi	924	6	4.3	359	24	ABU10530	Human secreted/tr
852	6	4.3	315	24	ABG25914	Aspergillus fumiga	925	6	4.3	360	21	ABP78133	N. gonorrhoeae ami
853	6	4.3	315	24	ABG26514	Aspergillus fumiga	926	6	4.3	361	21	ABW41628	Human ORFX ORF1392
854	6	4.3	318	20	AAW95502	C. acetobutylicum	927	6	4.3	361	21	AAW10109	Arabidopsis thalia
855	6	4.3	318	22	AAU38156	Salmonella typhi c	928	6	4.3	361	22	ABG82410	S. epidermidis ope
856	6	4.3	319	18	AAW14146	Human A33 antigen.	928	6	4.3	365	23	ABP69786	Human polypeptide
857	6	4.3	319	20	AAU23323	Amino acid sequenc	929	6	4.3	365	23	ABG02716	Human polypeptide
858	6	4.3	319	22	AAW365863	Human A33 protein	930	6	4.3	367	22	AAW21561	Novel human diagno
859	6	4.3	321	22	AAU34490	E. coli cellular p	931	6	4.3	370	22	AAU51676	T. neopolitana Xyn
860	6	4.3	321	22	AAW98356	Escherichia coli p	932	6	4.3	372	23	AAW79570	Propionibacterium
861	6	4.3	322	22	AAW98356	Dihydrodipicolinic	933	6	4.3	372	23	AAW79570	Propionibacterium
862	6	4.3	326	17	AAW06325	Bacillus thuringie	934	6	4.3	373	15	ABW48703	G-protein coupled
863	6	4.3	327	19	AAW60320	Bacillus thuringie	935	6	4.3	373	17	AAW02675	G-protein coupled
864	6	4.3	327	19	AAW60323	Bacillus thuringie	936	6	4.3	374	21	AAW05905	G-protein coupled
865	6	4.3	327	19	AAW90286	Human peptidase, H	937	6	4.3	374	21	ABG12962	Arabidopsis thalia
866	6	4.3	327	22	AAW03647	Human extracellular	938	6	4.3	375	24	ABP73019	Arabidopsis thalia
867	6	4.3	328	22	AAU35731	Helicobacter pylori	939	6	4.3	375	24	ABP70707	Arabidopsis thalia
868	6	4.3	331	20	AAU37504	Protein involved i	940	6	4.3	377	21	AAW20649	Arabidopsis thalia
869	6	4.3	331	22	AAU46431	Propionibacterium	941	6	4.3	377	21	AAW45918	Arabidopsis thalia
870	6	4.3	331	22	ABG18006	Propionibacterium	942	6	4.3	378	22	ABG03193	Novel human diagno
871	6	4.3	332	21	AAW55394	Novel human diagno	943	6	4.3	378	22	ABG03193	Novel human diagno
872	6	4.3	332	21	AAW55394	Arabidopsis thalia	944	6	4.3	378	23	ABW92716	Human polypeptide
873	6	4.3	332	22	AAW90554	C glutamicum prote	945	6	4.3	378	23	ABW92716	Herbicidally activ
874	6	4.3	332	23	AAU79516	Corynebacterium gl	946	6	4.3	380	17	AAW06326	M sterilia protein
875	6	4.3	332	23	AAU76428	Feline melanocorti	947	6	4.3	380	17	AAW06326	DHPS:chloroplast t
876	6	4.3	332	23	AAU76428	Canine melanocorti	948	6	4.3	380	21	AAW24234	Arabidopsis thalia
877	6	4.3	333	21	AAW30942	Arabidopsis thalia	949	6	4.3	380	21	AAW39915	Arabidopsis thalia
878	6	4.3	333	21	AAW30942	Streptococcus poly	950	6	4.3	380	21	AAW77934	A. Chaliana enviro
879	6	4.3	336	23	ABW62881	Human polypeptide	951	6	4.3	381	21	AAW93230	Herbicidally activ
880	6	4.3	337	22	ABG18204	Novel human diagno	952	6	4.3	381	21	AAW20525	Arabidopsis thalia
881	6	4.3	338	23	ABW57357	Mouse ischaemic co	953	6	4.3	381	22	AAU33416	Enterococcus faeca
882	6	4.3	339	20	AAW35649	Streptococcus poly	954	6	4.3	382	23	AAW75676	Human D1AR-V2R pol
883	6	4.3	340	23	ABP29857	Streptococcus poly	955	6	4.3	383	15	AAW56166	Neuroendocrine tum
884	6	4.3	340	23	ABU02808	S. pneumoniae type	956	6	4.3	383	24	ABU12064	Human NOV11a CG916
885	6	4.3	341	21	AAW55460	Arabidopsis thalia	957	6	4.3	384	22	AAW99128	Human NOV11b CG916
	6	4.3	341	21	AAW55460	Arabidopsis thalia	958	6	4.3	386	22	ABW63549	Rat G protein-coup
	6	4.3	341	21	AAW55460	Arabidopsis thalia	958	6	4.3	386	22	ABW63549	Drosophila melanog

959 4.3 388 13 AAR25698 Murine adrenergic
960 4.3 388 17 AAW05845 Fusarium oxysporum
961 4.3 388 21 AAG05673 Arabidopsis thalia
962 4.3 388 21 AAG08797 Arabidopsis thalia
963 4.3 388 21 AAG12961 Arabidopsis thalia
964 4.3 388 21 AAG17400 Arabidopsis thalia
965 4.3 388 21 AAG23445 Arabidopsis thalia
966 4.3 388 21 AAG27575 Arabidopsis thalia
967 4.3 388 22 ABB61443 Drosophila melanog
968 4.3 389 22 AAB62420 Human obesity prot
969 4.3 390 23 AAO21482 Mature human NGR2
970 4.3 395 24 ABU12114 Human protein mod
971 4.3 396 19 AAW56003 Trichomonas vagina
972 4.3 396 19 AAW56005 Trichomonas vagina
973 4.3 396 20 AAY03202 Amino acid sequenc
974 4.3 396 21 AAY96242 T. vaginalis homoc
975 4.3 396 22 AAG67257 Amino acid sequenc
976 4.3 396 22 AAB94593 Human protein sequ
977 4.3 396 22 AAB67241 T.vaginalis homocy
978 4.3 396 22 AAE09318 Maize arsenite tra
979 4.3 396 23 AAB62789 Protein fragment #
980 4.3 397 21 AAG51570 Arabidopsis thalia
981 4.3 397 22 AAG08725 Novel human diagno
982 4.3 399 21 AAG20648 Arabidopsis thalia
983 4.3 399 21 AAG20924 Arabidopsis thalia
984 4.3 399 21 AAG45917 Arabidopsis thalia
985 4.3 400 15 AAS49392 Murine beta-3 adre
986 4.3 400 19 AAW50283 Canine herpes viru
987 4.3 401 14 AAR40800 TGF-beta-like cion
988 4.3 401 21 AAG12960 Arabidopsis thalia
989 4.3 401 24 AAE33486 Human REMAP-17 pr
990 4.3 402 21 AAB14800 Erysielothrix rhu
991 4.3 402 21 AAG10108 Arabidopsis thalia
992 4.3 402 21 AAG30849 Arabidopsis thalia
993 4.3 402 23 ABB07787 E rhusiopathiae pr
994 4.3 402 23 ABB08869 Erysielothrix rhu
995 4.3 403 20 AAY03201 Amino acid sequenc
996 4.3 403 21 AAG48512 Arabidopsis thalia
997 4.3 403 21 AAY96241 T. vaginalis homoc
998 4.3 403 21 AAY76757 T. vaginalis homoc
999 4.3 403 22 AAB67240 T.vaginalis homocy
1000 4.3 404 21 AAG20647 Arabidopsis thalia

ALIGNMENTS

RESULT 1
ABP53714
ID ABP53714 standard; Protein; 141 AA.
XX
AC ABP53714;
XX
DT 23-DEC-2002 (first entry)
XX
DE Babesia canis BcVir15 15kD protein SEQ ID NO:2.
XX
KW Babesia canis; BcVir15; 15kD protein; BcVir32; 32kD protein; infection;
KW antiparasitic; immunostimulant; vaccine.
XX
OS Babesia canis.
XX
PN EPI238983-A1.
XX
PD 11-SEP-2002.
XX
PF 04-MAR-2002; 2002EP-0075830.
XX
PR 06-MAR-2001; 2001EP-0200816.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Schettlers TPM, Carcy BPD, Drakulovski PR, Gorenflot AF;

XX WPI: 2002-724917/79.
DR N-FSDB; ABQ82649.
XX
XX Novel Babesia canis associated protein and nucleic acid encoding the
PT protein, useful in a vaccine and in the manufacture of vaccines for
PT combating Babesia canis infections
XX
XX Claim 1; Fig 2; 4lpp; English.
XX
CC The present invention describes a Babesia canis associated protein (I),
CC comprising a BcVir15 protein of 15 kD molecular weight (MW) and having
CC a sequence of at least 80% homology to a sequence (ABP53714) of 141
CC amino acids, or a BcVir32 protein of 32 kD MW and having a sequence of
CC at least 80% homology to a sequence (ABP53715) of 285 amino acids, or
CC their immunogenic fragments. (I) have antiparasitic and immunostimulant
CC activities, and can be used in vaccines. (I) can also be used for the
CC preparation of a vaccine for combating B. canis infections. (I) is also
CC useful in a diagnostic test for the detection of antibodies against
CC B. canis associated antigenic material. The present sequence represents
CC BcVir15 from the present invention.
XX
SQ Sequence 141 AA;

Query Match 100.0%; Score 141; DB 23; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.2e-137; Indels 0; Gaps 0;
Matches 141; Conservative 0; Mismatches 0;
QY 1 MESTSTTNFVAENRPTFGSTFDVMEALLRVKSSERLALAGMCGHRVLPGTGASA 60
DB 1 MESTSTTNFVAENRPTFGSTFDVMEALLRVKSSERLALAGMCGHRVLPGTGASA 60
QY 61 IAAVTTPKASMKLKP RPPOSTKSPELRELSRKIRENMKTIQSARVNHRLPEGHPLLE 120
DB 61 IAAVTTPKASMKLKP RPPOSTKSPELRELSRKIRENMKTIQSARVNHRLPEGHPLLE 120
QY 121 KRAEYFRHLRSLKSGQVNRLLI 141
DB 121 KRAEYFRHLRSLKSGQVNRLLI 141
RESULT 2
ABP53715
ID ABP53715 standard; Protein; 285 AA.
XX
AC ABP53715;
XX
DT 23-DEC-2002 (first entry)
XX
DE Babesia canis BcVir32 32kD protein SEQ ID NO:4.
XX
KW Babesia canis; BcVir15; 15kD protein; BcVir32; 32kD protein; infection;
KW antiparasitic; immunostimulant; vaccine.
XX
OS Babesia canis.
XX
PN EPI238983-A1.
XX
PD 11-SEP-2002.
XX
PF 04-MAR-2002; 2002EP-0075830.
XX
PR 06-MAR-2001; 2001EP-0200816.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Schettlers TPM, Carcy BPD, Drakulovski PR, Gorenflot AF;

PT combating Babesia canis infections -
PS Claim 2; Fig 3; 41pp; English.
XX
CC The present invention describes a Babesia canis associated protein (I),
CC comprising a BcVir15 protein of 15 kD molecular weight (MW) and having
CC a sequence of at least 80% homology to a sequence (ABP53714) of 141
CC amino acids, or a BcVir12 protein of 32 kD MW and having a sequence of
CC at least 80% homology to a sequence (ABP53715) of 285 amino acids, or
CC their immunogenic fragments. (I) have antiparasitic and immunostimulant
CC activities, and can be used in vaccines. (I) can also be used for the
CC preparation of a vaccine for combating B. canis infections. (I) is also
CC useful in a diagnostic test for the detection of antibodies against
CC B. canis associated antigenic material. The present sequence represents
XX BcVir12 from the present invention.
SQ Sequence 285 AA;
Query Match 89.4%; Score 126; DB 23; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.4e-121; Mismatches 0; Indels 0; Gaps 0;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESTTTTNFVAVENRPTFGETDVNREALLRVKSSERLAMLALAGMCHRVLPQTGASA 60
DB 1 MESTTTTNFVAVENRPTFGETDVNREALLRVKSSERLAMLALAGMCHRVLPQTGASA 60
QY 61 IAATVTPGASMKLAPPRQSTKSPRLRLSKIREMKNKTSQESARVNHRLPEGHPLLE 120
DB 61 IAATVTPGASMKLAPPRQSTKSPRLRLSKIREMKNKTSQESARVNHRLPEGHPLLE 120
QY 121 KRAEYF 126
DB 121 KRAEYF 126

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX Claim 1; Fig 2; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related diseases, cell
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX Sequence 16 AA;
SQ
Query Match 5.0%; Score 7; DB 24; Length 16;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VLPQTGA 58
DB 5 VLPQTGA 11
RESULT 4
AAU46323
ID AAU46323 standard; Protein; 88 AA.
AC AAU46323;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #7219.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
FA (CORI-) CORIXA CORP.
XX

PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59531.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 7518; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 88 AA;
SQ
Query Match 5.0%; Score 7; DB 22; Length 88;
Best Local Similarity 100.0%; Pred. No. 36;
Matches. 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 111 RLPEGHP 117
Db 66 RLPEGHP 72
RESULT 5
AAM85765
ID AAM85765 standard; Protein; 97 AA.
XX
AC AAM85765;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:13358.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WC200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR
07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214896.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225758.
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PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226888.
PR 22-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.

PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0245474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
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PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
DR N-PSDB; AAK58546.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Claim 11; SEQ ID NO 13358; 3071pp + Sequence Listing; English.
PS
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK52170 to AAK51921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent.
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX
SQ Sequence 97 AA;

Query Match 5.0%; Score 7; DB 22; Length 97;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RVLPGTG 57
|||
Db 65 RVLPGTG 71

RESULT 6
ABP09535
ID ABP09535 standard; Protein; 103 AA.
XX
AC ABP09535;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:19052.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
XX OS Homo sapiens.
XX
XX WO200192523-A2.
XX
XX 06-DEC-2001.
XX
XX 29-MAY-2001; 2001WO-US10836.
XX
XX 30-MAY-2000; 2000US-206132P.
XX
XX 29-AUG-2000; 2000US-228716P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach MD;
XX
XX WPI; 2002-106308/14.
XX
XX N-PSDB; ABN25287.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders -
XX
XX Disclosure; SEQ ID 19052; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated

CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 XX
 SQ Sequence 103 AA;
 Query Match 5.0%; Score 7; DB 23; Length 103;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LLRVKSS 35
 Db 10 LLRVKSS 16
 |||||

RESULT 7
 ID AAO10778
 AC AAO10778 standard; Protein; 141 AA.

XX
 AC AAO10778;
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 24670.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

OS WO200164835-A2.

PN 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AA190709.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 141 AA;

Query Match 5.0%; Score 7; DB 22; Length 141;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 LKSQGVN 138
 Db 24 LKSQGVN 30
 |||||

RESULT 8
 ABP31776
 ID ABP31776 standard; Protein; 157 AA.

XX
 AC ABP31776;

DT 08-JUL-2002 (first entry)

XX Human ORP749 protein, SEQ ID NO:1498.

XX Human; ORP; open reading frame; ORFX; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
 KW vasotrophic; antipsoriatic; antidiabetic; cytostatic; neurotropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide.

XX Homo sapiens.

OS WO200190366-A2.

PN 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17076.

XX 24-MAY-2000; 2000US-206690P.

XX (CURA-) CURAGEN CORP.

XX Leach MD, Shinkets RA;

XX WPI; 2002-106200/14.

DR N-PSDB; ABN75802.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation -

XX Claim 10; Page 640; 2508pp; English.

XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins

designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN7587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and polypeptides, methods of screening individuals for a predisposition or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.

Query Match 5.0%; Score 7; DB 23; Length 157;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 LRLSKQ 135
Db 132 LRLSKQ 138
|||||

RESULT 9
AB568671
ID ABB68671 standard; Protein; 159 AA.
XX ABB68671;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 32805.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX

WPI; 2001-656860/75.
DR N-PSDB; ABL12774.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
PT
PT
XX
XX Disclosure; SEQ ID NO 32805; 21pp + Sequence Listing; English.
PS
CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
CC
CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
XX

Sequence 159 AA;
Query Match 5.0%; Score 7; DB 22; Length 159;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESTSTTT 8
Db 29 ESTSTTT 35
|||||

RESULT 10
AAU41908
ID AAU41908 standard; Protein; 202 AA.
XX
XX AAU41908;
AC
XX 13-FEB-2002 (first entry)
DT
XX
XX Propionibacterium acnes immunogenic protein #2804.
DE
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
KW
XX
XX Propionibacterium acnes.
OS
XX
XX WO200181581-A2.
FN
XX
XX 01-NOV-2001.
PD
XX
XX 20-APR-2001; 2001WO-US12865.
PF
XX
XX 21-APR-2000; 2000US-199047P.
PR
XX 02-JUN-2000; 2000US-208841P.
PR
XX 07-JUL-2000; 2000US-216747P.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
PI
XX
XX WPI; 2001-616774/71.
DR
XX N-PSDB; AAS59515.
DR
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
PT
PT
XX
XX Example 1; SEQ ID No 3103; 1069pp; English.
PS
XX

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 202 AA;

Query Match 5.0%; Score 7; DB 22; Length 202;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 CGHRVLP 54
Db 125 CGHRVLP 131
|||||

RESULT 11
ABB67442
ID ABB67442 standard; Protein; 203 AA.

XX ABB67442;
AC ABB67442;
XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 29118.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.
OS WO200171042-A2.
XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
XX N-PSDB; ABL11545.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT

XX Disclosure; SEQ ID NO 29118; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 203 AA;

Query Match 5.0%; Score 7; DB 22; Length 203;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LLRVKSS 35
Db 192 LLRVKSS 198
|||||

RESULT 12
AAB86467
ID AAB86467 standard; Protein; 214 AA.

XX AAB86467;
AC AAB86467;
XX 26-OCT-2001 (first entry)

XX Cryptocodinium sp elongase protein fragment from clone Cc_PSE1.
DE Elongase; plant; transgenic plant; fatty acid; PUFA; oil; lipid; food;
KW polyunsaturated fatty acid; fodder; cosmetic; pharmaceutical.
XX Cryptocodinium sp.

XX WO200159128-A2.
XX 16-AUG-2001.
PD 08-FEB-2001; 2001WO-EP01346.

XX 09-FEB-2000; 2000DE-1005973.
PR 17-MAY-2000; 2000DE-1023893.
PR 19-DEC-2000; 2000DE-1063387.

XX (BADI) BASF AG.
XX Heinz E, Zank T, Zaehring U, Lerchl J, Renz A;
PI WPI; 2001-529842/58.
XX N-PSDB; AAB48739.

XX New elongase gene extends 16, 18 and 20 carbon fatty acids, useful to
PT manipulate plants to produce polyunsaturated fatty acids for the
PT foodstuffs, cosmetics and pharmaceutical industries -
XX Claim 2c; Page 129-130; 135pp; German.

XX This invention describes a novel isolated nucleic acid from a plant or
CC algae which encodes a polypeptide which extends a C₁₆, C₁₈ or C₂₀
CC fatty acid having at least two double bonds by at least two carbon atoms.
CC The products of the invention can be used to produce polyunsaturated
CC fatty acids (PUFAs) in the form of oils, lipids or fatty acids in a
CC method which comprises breeding organisms e.g. transgenic plants
CC containing the above nucleic acids, constructs or vectors encoding a
CC polypeptide which extends a C₁₆, C₁₈ or C₂₀ fatty acid having at
CC least two double bonds by at least two carbon atoms, under PUFA forming
CC conditions. The oils, lipids or fatty acid compositions produced by the
CC invention are used in fodder, food, cosmetics and pharmaceuticals. The
CC invention is more efficient at producing polyunsaturated fatty acids in a
CC broad spectrum of plants than prior art. This sequence represents the
CC Cryptocodinium sp. elongase protein isolated from clone Cc_PSE1 which
CC is described in the method of the invention.

3Q Sequence 214 AA;
Query Match 5.0%; Score 7; DB 22; Length 214;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2Y 88 RELSRKI 94
| | | | |
3b 192 RELSRKI 198
| | | | |
RESULT 13
ID ABG26750 standard; Protein; 236 AA.
AC ABG26750;
XX
DT 18-FEB-2002 (first entry)
DE
XX
XX Novel human diagnostic protein #26741.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX N-PSDB; AAS90937.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 57109; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 236 AA;

Query Match 5.0%; Score 7; DB 22; Length 236;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 LAMLRAL 44
| | | | |
Db 112 LAMLRAL 118
| | | | |
RESULT 14
ID ABB12033 standard; peptide; 236 AA.
XX
XX ABB12033;
XX
XX 11-JAN-2002 (first entry)
XX
XX Human novel protein, SEQ ID NO:2403.
XX
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.
XX
XX Homo sapiens.
XX
XX WO200157188-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US03800.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
XX N-PSDB; ABA09277.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
XX treating or ameliorating a medical condition in a mammalian subject
XX e.g. arthritis and cancer -
XX
XX Claim 20; Page 300; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell
XX differentiation activities; stem cell growth factor activity;
XX haematopoiesis regulatory activity; tissue growth activity;
XX immunomodulatory activity; activin- or inhibin-related activities;
XX chemotactic or chemokinetic activities; haemostatic, thrombotic or
XX thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC can also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

SQ Sequence 236 AA;
 Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 PELRELS 91
 Db |||||
 8 PELRELS 14

RESULT 15
 AAM80027
 ID AAM80027 standard; Protein; 236 AA.

AC AAM80027;
 DT 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 3673.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.
 OS
 XX WO200157190-A2.
 FN
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US04098.
 PF
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI: 2001-476283/51.
 DR N-PSDB; AAK53160.

XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 410; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX SQ Sequence 236 AA;

Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 PELRELS 91
 Db |||||
 8 PELRELS 14

RESULT 16
 AAM80028
 ID AAM80028 standard; Protein; 236 AA.

AC AAM80028;
 DT 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 3674.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.
 OS
 XX WO200157190-A2.
 FN
 XX 09-AUG-2001.
 PD
 XX 05-FEB-2001; 2001WO-US04098.
 PF
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI: 2001-476283/51.
 DR N-ESDB; AAK53161.

PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 XX Claim 20; Page 410; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and/or
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 XX Sequence 236 AA;
 SQ

Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 PELRELS 91
 Db 8 PELRELS 14

RESULT 17
 AAM41648
 ID AAM41648 standard; Protein; 236 AA.
 XX
 AC AAM41648;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6579.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US34263.

PF 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Dirmannac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB; AAI60804.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 XX Example 2; SEQ ID NO 6579; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAW42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression.
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 236 AA;
 SQ

Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 PELRELS 91
 Db 8 PELRELS 14

RESULT 18

AAV83184

ID AAV83184 standard; peptide; 293 AA.

XX
 AC AAV83184;

XX 24-JUL-2000 (first entry)

XX Melanocortin receptor MC4 Factor Xa cleavage product.

XX Membrane polypeptide; lipid matrix; synthesis; ligation;
 KW chemoselective ligation; fluorescence resonance energy transfer;
 KW FRET; chromophore; ligand; receptor domain; drug screening;
 KW diagnosis; ion channel; melanocortin receptor; MC4.

XX Synthetic.

OS Homo sapiens.

XX WO200012536-A2.

PN 09-MAR-2000.

PD 26-AUG-1999; 99WO-US19542.

PF 31-AUG-1998; 98US-0144964.

PR 05-MAR-1999; 99US-0263971.

XX (GRYP-) GRYPHON SCI.

XX Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;
 PI WPI: 2000-270792/23.

XX Selectively labeled membrane peptides, useful e.g. for detecting ligand
 PT binding to receptors and in drug screening, are prepared, in lipid
 PT matrix, by reaction between amino acid residues
 XX
 XX Example 11; Page 70; 120pp; English.

CC New methods are described by which membrane polypeptides can be
CC labelled. The method comprises chemoselective chemical ligation of
CC the membrane polypeptide which is incorporated in a lipid matrix,
CC and a ligation label. Both contain an amino acid having an
CC unprotected reactive group that together undergo chemoselective
CC ligation to form a covalent bond. The method can be used to label
CC folded polypeptides embedded in a lipid membrane, by treating the
CC polypeptide with a reagent that cleaves specifically adjacent to an
CC amino acid with an unprotected reactive group, and then ligating the
CC cleaved polypeptide with the ligation label. The ligation label can
CC be a chromophore, thus ligand binding to membrane bound polypeptides
CC can be detected by contacting a membrane bound polypeptide comprising
CC a chromophore, with the ligand under investigation and screening for
CC binding in an assay characterized by detecting fluorescence resonance
CC energy transfer (FRET) between the chromophore and a second
CC chromophore, the chromophores comprising a donor and acceptor pair of
CC a resonance energy transfer system. The methods are used for lipid
CC matrix-assisted chemical ligation and synthesis of membrane
CC polypeptides. Labeled membrane polypeptides are used to detect ligand
CC binding and the identification of receptor domains, e.g. for
CC structure/activity studies. They can also be used in drug screening,
CC selection or design, and for diagnosis. The methods are particularly
CC used for fluorescent resonance energy transfer (FRET) analysis of
CC previously inaccessible membrane polypeptides. The method allows
CC site-specific incorporation of labels during polypeptide synthesis
CC and analysis of previously inaccessible membrane proteins. A
CC Melanocortin receptor MC4 which also comprises a factor Xa cleavage
CC site (AA83182) can be cleaved with Factor Xa to give a
CC C-terminal alpha-thioester modified MC4 receptor ligation label
CC (AA83183) and this MC4 receptor membrane polypeptide cleavage product
CC Chemical ligation of cleaved MC4 in alternative membrane patches or
CC micelles to an MC4 ligation label produces the synthetic labeled
CC MC4 product (AA83183).

XX Sequence 293 AA;
SQ

Query Match 5.0%; Score 7; DB 21; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPQTGA 58
Db 189 VLPQTGA 195

RESULT 19
ABG71866
ID ABG71866 standard; protein; 293 AA.
XX
AC ABG71866;
XX
DT 15-JAN-2003 (first entry)
XX
DE Melanocortin receptor, MC4, factor Xa cleavage product.
XX
KW Melanocortin receptor; membrane protein; MC4; factor Xa; lipid matrix;
KW chemoselective chemical ligation; CCL; ligation label; ligand binding;
KW FRET; fluorescence resonance energy transfer; receptor; human.
XX
OS Homo sapiens.
XX
PN US6451543-B1.
XX
PD 17-SEP-2002.
XX
PF 26-AUG-1999; 99US-0384302.
XX
PR 31-AUG-1998; 98US-0144964.
PR 05-MAR-1999; 99US-0263971.
XX
PA (GRYP-) GRYPHON SCI.
XX
PI Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;

XX WPI; 2003-045578/04.
DR Chemoselective chemical ligation of membrane polypeptides useful for
XX assaying ligand binding to membrane polypeptides, involves covalently
PT binding polypeptides incorporated in a lipid matrix with ligation
PT labels -
XX
PS Example 11; Column 48; 52pp; English.
XX
CC The invention relates to chemoselective chemical ligation (CCL) of a
CC membrane polypeptide, (M1) involves contacting (under CCL conditions):
CC (a) polypeptide (I) incorporated in lipid matrix, comprising first
CC amino acid (A1) having unprotected reactive group; (b) with ligation
CC label (I1) comprising second amino acid (A2) having unprotected reactive
CC group, (A2 is capable of CCL with A1, and contacting (I) with (I1) causes
CC a covalent bond to be formed between unprotected reactive groups of A1
CC and A2). Also included are a composition comprising an integral membrane
CC polypeptide embedded in a lipid matrix and at least one non-naturally
CC occurring amino acid comprising a unprotected reactive group; and a
CC CCL with (I1) having a compatible unprotected reactive group; and a
CC composition comprising a membrane polypeptide embedded in a lipid matrix
CC (the membrane polypeptide has at least two amino acid residues
CC covalently joined through a non-natural backbone bond). The method
CC is used for chemoselective chemical ligation of a folded membrane
CC polypeptide, or an integral or transmembrane polypeptide, where the
CC transmembrane polypeptide is a receptor. The method is useful for
CC detecting a ligand that directly or indirectly interacts with a folded
CC membrane polypeptide embedded in a lipid matrix. This
CC method is particularly useful for diagnostic assays, screening new
CC compounds for drug development, and other structural and functional
CC assays that employ binding of a ligand to a pre-folded membrane
CC polypeptide. (M1) and (I1) can be used to assay ligand binding to
CC membrane polypeptides and domains comprising a receptor, and thus are
CC extremely useful for structure/function studies, drug
CC screening/selection/design and diagnostics, etc. including
CC high-throughput applications. The methods and compositions are
CC particularly suited for fluorescence resonance energy transfer (FRET)
CC analyses of previously inaccessible membrane polypeptides. The
CC present sequence is the melanocortin receptor, MC4, factor Xa
CC cleavage product, used to demonstrate the method of the invention.

XX Sequence 293 AA;
SQ

Query Match 5.0%; Score 7; DB 24; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPQTGA 58
Db 189 VLPQTGA 195

RESULT 20
AAU08750
ID AAU08750 standard; Protein; 311 AA.
XX
AC AAU08750;
XX
DT 28-DEC-2001 (first entry)
XX
DE Human melanocortin-4 receptor (MC4R) polypeptide.
XX
KW Melanocortin-4 receptor; MC4R; meat quality; drip loss; marbling; sheep;
KW pig; cow; chicken; animal breeding; pH; polymorphism; slaughter; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 298 /label= OTHER
FT /note= "OTHER= any amino acid"
XX

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DR  N-PSDB; AAF44834.
XX
XX  Novel defender against cell death polynucleotide useful for modulating
XX  programmed cell death pathway and specific development pathways in
XX  forestry plant -
XX
XX  Claim 22; Pages 131-132; 142pp; English.
XX
XX  The present invention relates to coding sequences (see AAF44740-F44840
XX  and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in
XX  programmed cell death (PCD; apoptosis). The coding sequences and proteins
XX  of the present invention are useful for modulating a PCD or cell death
XX  pathway and various developmental pathways in a forestry plant, by
XX  stably incorporating one of the present coding sequences into the genome
XX  of the forestry plant, where the coding sequence provides a PCD pathway
XX  that is not present in a native form of the forestry plant.
XX
XX  Sequence 320 AA;
XX
XX  Query Match 5.0%; Score 7; DB 22; Length 320;
XX  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 126 FRLHLSL 132
XX  |||||
XX  Db 252 FRLHLSL 258
XX
XX  RESULT 22
XX  AAW19704
XX  ID AAW19704 standard; Protein; 332 AA.
XX  AC AAW19704;
XX  XX
XX  DT 19-AUG-1997 (first entry)
XX  DE Melanocortin-4 receptor.
XX  XX
XX  XX Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;
XX  KW pro-opiomelanocortin; adrenal cortical function; behaviour; learning;
XX  KW memory; cardiovascular system; analgesia; thermoregulation; prolactin;
XX  KW neurohumoral agent; biogenic amine.
XX  OS Homo sapiens.
XX  XX
XX  XX US5622860-A.
XX  XX
XX  XX 22-APR-1997.
XX  XX
XX  XX 17-FEB-1994; 94US-0200711.
XX  XX
XX  XX 17-FEB-1994; 94US-0200711.
XX  XX (UNMI ) UNIV MICHIGAN.
XX  XX
XX  XX Gantz I, Yamada T;
XX  XX WPI, 1997-244394/22.
XX  XX N-PSDB; AAT68790.
XX  XX
XX  XX Nucleic acid molecules encoding melanocortin receptors - useful to
XX  XX transfect mammalian cells lacking endogenous receptors to induce
XX  XX their expression
XX  XX
XX  XX Claim 4; Column 43-46; 58pp; English.
XX  XX
XX  XX AAW19703-W19707 represent the human and mouse melanocortin (MC)
XX  XX receptors. This sequence represents the MC4R, expressed primarily in
XX  XX brain, but absent in the adrenal cortex, melanocytes and placenta. The
XX  XX gene encoding this sequence is located at chromosome locus 18q21.3. MCs
XX  XX are products of pro-opiomelanocortin post-translational processing, and
XX  XX are known to have a broad array of physiological actions. MCs are known
XX  XX to have effects on adrenal cortical functions and on melanocytes as well

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as affecting behaviour, learning, memory, control of the cardiovascular system, analgesia, thermoregulation and the release of other neurohumoral agents (such as prolactin and biogenic amines). The nucleic acids can be used to transfect mammalian cells lacking endogenous MC receptors to induce their expression. These sequences can also be used to screen and identify drugs which specifically react with MCRs on the surface of a cell. The drugs can then be used for treating diseases which have MCRs implicated as one of their causes. Vectors containing these sequences can also be used to treat the diseases.

Query Match 5.0%; Score 7; DB 18; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 23
AAW79687
ID AAW79687 standard; Protein; 332 AA.
AC AAW79687;
DT 17-DEC-1998 (first entry)
DE Melanocortin-4 receptor.
KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain; adrenal cortex; melanocyte; placenta.
XX Homo sapiens.
XX US5817787-A.
XX 06-OCT-1998.
XX 23-APR-1997; 97US-0842045.
XX 17-FEB-1994; 94US-0200711.
XX 27-JUN-1996; 96US-0672109.
XX 23-APR-1997; 97US-0842045.
XX (UNMI) UNIV MICHIGAN.
XX Gantz I, Yamada T;
XX WPI; 1998-556471/47.
XX N-PSDB; AAV62352.
XX DNA encoding melanocortin-5 receptor - useful in hybridisation assays for melanocortin-5 receptor nucleic acids
XX Disclosure; Column 43-46; 58pp; English.

The present sequence represents the human melanocortin-4 (MC4) receptor, the gene of which has been localised to chromosome 18q21.3. This receptor is activated by both the amino and carboxyl terminal end amino acids of melanocortins and has been found to be expressed primarily in the brain and is absent from the adrenal cortex, melanocytes and placenta. The DNA sequence that produces this polypeptide was identified by using oligonucleotides constructed from previously identified receptors MC1 and MC3, this was performed by using these oligonucleotides to search genomic DNA for other members of the receptor family. These genes and their products may be used to provide therapeutic vehicles for the treatment of processes involving the function of melanocortin receptors.

Query Match 5.0%; Score 7; DB 18; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 23
AAW79687
ID AAW79687 standard; Protein; 332 AA.
AC AAW79687;
DT 17-DEC-1998 (first entry)
DE Melanocortin-4 receptor.
KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain; adrenal cortex; melanocyte; placenta.
XX Homo sapiens.
XX US5817787-A.
XX 06-OCT-1998.
XX 23-APR-1997; 97US-0842045.
XX 17-FEB-1994; 94US-0200711.
XX 27-JUN-1996; 96US-0672109.
XX 23-APR-1997; 97US-0842045.
XX (UNMI) UNIV MICHIGAN.
XX Gantz I, Yamada T;
XX WPI; 1998-556471/47.
XX N-PSDB; AAV62352.
XX DNA encoding melanocortin-5 receptor - useful in hybridisation assays for melanocortin-5 receptor nucleic acids
XX Disclosure; Column 43-46; 58pp; English.

Query Match 5.0%; Score 7; DB 19; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 24
AAW37831
ID AAW37831 standard; Protein; 332 AA.
XX AAW37831;
DT 28-JUL-1998 (first entry)
DE Human melanocortin-4 receptor.
KW Human melanocortin-4 receptor gene; metabolic disorder; agonist; antagonist; feeding; eating disorder; anorexia; obesity; cachexia; cancer; inhibition; melanocortin receptor; MCR.
XX Homo sapiens.
XX WO9810068-A2.
XX 12-MAR-1998.
XX 04-SEP-1997; 97WO-US15565.
XX 04-SEP-1996; 96US-0706281.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Boston BA, Chen W, Cone RD, Fan W, Kesterton RA;
XX Lu D;
XX WPI; 1998-193618/17.
XX N-PSDB; AAV19142.
XX Identifying melanocortin receptor agonists and antagonists - using a panel of recombinant mammalian cells expressing alpha-melanocyte stimulating hormone, ACTH, MC-3, MC-4 and MC-5 receptors
XX Example 2F; Fig 6A-B; 121pp; English.

This is the amino acid sequence of the human melanocortin-4 receptor (MCR-4). The MCR agonists and antagonists can be used for modifying feeding behaviour in an animal. The antagonists can be used for stimulating feeding while the agonists can be used for inhibiting feeding. They can be used for the treatment of eating disorders such as anorexia and obesity, and other pathological weight and eating-related disorders. They can also be used to treat failure to thrive disorders and disease-related cachexia, such as occurs in cancer patients, as well as other metabolic disorders.

Query Match 5.0%; Score 7; DB 19; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 25
AAW42377
ID AAW42377 standard; Protein; 332 AA.
XX AAW42377;
AC AAW42377;

KX 25-MAR-2003 (updated)
DT 08-JUN-1998 (first entry)
XX Homo sapiens mutant melanocortin 4 receptor Ile137Thr.
DE
KX Melanocortin 4 receptor; MC4-R gene; body weight disorder;
KW Melanocortin 4 receptor; obesity; cachexia; Val102Ile; mutant.
XX treatment; obesity; anorexia; cachexia; Val102Ile; mutant.
DS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 137..137
FT /note= "Ile137Thr mutation from wild-type"
XX
PN WO9747316-A1.
XX
PD 18-DEC-1997.
XX
PF 09-JUN-1997; 97WO-US09969.
XX
PR 10-JUN-1996; 96US-0662560.
XX
PR 08-JAN-1997; 97US-0780749.
XX
PR 06-JUN-1997; 97US-0870511.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Gu W, Huszar D, Lee F;
XX WPI; 1998-052026/05.
XX N-PSDB; AAV03251.
XX
XX Drug screening assays to identify compounds for body weight disorder
PT treatment - e.g. obesity, anorexia and cachexia, using melanocortin
PT 4 receptor as target
XX
PS Disclosure; Fig 11; 11lpp; English.
XX
CC The sequence is that of a mutant melanocortin 4 receptor (MC4-R),
CC the mutation is the Ile137Thr mutation. The sequence can be used in the
CC generation of drug screening assays to identify compounds which could
CC be used in the treatment of body weight disorders e.g. obesity, anorexia
CC and cachexia. Specific compounds include agonists or antibodies that
CC bind and activate the MC4-R to induce weight loss, an antibody or
CC extracellular domain of the MC4-R that inhibits MC4-R activation and
CC therefore induces weight gain or an oligonucleotide that inhibits
CC translation by encoding an antisense or ribozyme molecule that targets
CC MC4-R transcripts or by forming a triple helix with the MC4-R gene
CC promoter to induce weight gain.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 332 AA;
XX
Query Match 5.0%; Score 7; DB 19; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 52 VLPQTGA 58
Db 228 VLPQTGA 234
XX
RESULT 26
AAW42378
ID AAW42378 standard; Protein; 332 AA.
XX
XX AAW42378;
XX
XX 25-MAR-2003 (updated)
DT 08-JUN-1998 (first entry)
XX
DE Homo sapiens mutant melanocortin 4 receptor Val102Ile.
XX

KX Melanocortin 4 receptor; MC4-R gene; body weight disorder;
KW treatment; obesity; anorexia; cachexia; Val102Ile; mutant.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 102..102
FT /note= "Val102Ile mutation from wild-type"
XX
PN WO9747316-A1.
XX
PD 18-DEC-1997.
XX
PF 09-JUN-1997; 97WO-US09969.
XX
PR 10-JUN-1996; 96US-0662560.
XX
PR 08-JAN-1997; 97US-0780749.
XX
PR 06-JUN-1997; 97US-0870511.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Gu W, Huszar D, Lee F;
XX WPI; 1998-052026/05.
XX N-PSDB; AAV03252.
XX
XX Drug screening assays to identify compounds for body weight disorder
PT treatment - e.g. obesity, anorexia and cachexia, using melanocortin
PT 4 receptor as target
XX
PS Disclosure; Fig 12; 11lpp; English.
XX
CC The sequence is that of a mutant melanocortin 4 receptor (MC4-R),
CC the mutation is the Val102Ile mutation. The sequence can be used in the
CC generation of drug screening assays to identify compounds which could
CC be used in the treatment of body weight disorders e.g. obesity, anorexia
CC and cachexia. Specific compounds include agonists or antibodies that
CC bind and activate the MC4-R to induce weight loss, an antibody or
CC extracellular domain of the MC4-R that inhibits MC4-R activation and
CC therefore induces weight gain or an oligonucleotide that inhibits
CC translation by encoding an antisense or ribozyme molecule that targets
CC MC4-R transcripts or by forming a triple helix with the MC4-R gene
CC promoter to induce weight gain.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 332 AA;
XX
Query Match 5.0%; Score 7; DB 19; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 52 VLPQTGA 58
Db 228 VLPQTGA 234
XX
RESULT 27
AAW42379
ID AAW42379 standard; Protein; 332 AA.
XX
XX AAW42379;
XX
XX 25-MAR-2003 (updated)
DT 08-JUN-1998 (first entry)
XX
DE Homo sapiens mutant melanocortin 4 receptor Thr112Met.
XX
KW Melanocortin 4 receptor; MC4-R gene; body weight disorder;
KW treatment; obesity; anorexia; cachexia; Thr112Met; mutant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

FT Misc-difference 112..112
 FT /note= "Thr112Met mutation from wild-type"

PN WC9747316-A1.
 XX 18-DEC-1997.
 XX 09-JUN-1997; 97WO-US09969.
 XX 10-JUN-1996; 96US-0662560.
 PR 08-JAN-1997; 97US-0780749.
 PR 06-JUN-1997; 97US-0870511.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Gu W, Huszar D, Lee F;
 XX WPI; 1998-052026/05.
 DR N-PSDB; AAW42379.
 XX Drug screening assays to identify compounds for body weight disorder
 PT treatment - e.g. obesity, anorexia and cachexia, using melanocortin
 PT 4 receptor as target
 XX Disclosure; Fig 13; 11lpp; English.

XX The sequence is that of a mutant melanocortin 4 receptor (MC4-R),
 CC the mutation is the Thr112Met mutation. The sequence can be used in the
 CC generation of drug screening assays to identify compounds which could
 CC be used in the treatment of body weight disorders e.g. obesity, anorexia
 CC and cachexia. Specific compounds include agonists or antibodies that
 CC bind and activate the MC4-R to induce weight loss, an antibody or
 CC extracellular domain of the MC4-R that inhibits MC4-R activation and
 CC therefore induces weight gain or an oligonucleotide that inhibits
 CC translation by encoding an antisense or ribozyme molecule that targets
 CC MC4-R transcripts or by forming a triple helix with the MC4-R gene
 CC promoter to induce weight gain.
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 332 AA;
 SQ Query Match 5.0%; Score 7; DB 19; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 52 VLPQTGA 58
 DB 228 VLPQTGA 234

RESULT 28
 AAW33724
 ID AAW33724 standard; Protein; 332 AA.
 XX AAW33724;
 XX 30-APR-1998 (first entry)
 DE Human melanocortin-4 (MC4) receptor.
 XX Melanocortin receptor; ligand; MC4; human.

XX Homo sapiens.
 XX US5703220-A.
 XX 30-DEC-1997.
 XX 27-JUN-1996; 96US-0671525.
 XX 17-FEB-1994; 94US-0200711.
 XX 27-JUN-1996; 96US-0671525.

PA (UNMI) UNIV MICHIGAN.
 XX Gantz I, Yamada T;
 XX WPI; 1998-076484/07.
 DR N-PSDB; AAV06400.
 XX DNA encoding human melanocortin-4 receptor - and cells useful in
 PT assay for MC4 receptor ligands
 XX Claim 1; Columns 43-46; 59pp; English.
 XX This is a human melanocortin receptor-4 (MC4). The MC4 receptor of this
 CC invention is activated by amino acids in the carboxyl and amino terminal
 CC portions of the heptapeptide sequence shared by all the melanocortin
 CC peptides. MC4 is expressed primarily in brain and is notably absent in
 CC the adrenal cortex, melanocytes and placenta. The MC4 receptor gene was
 CC localised to chromosome loci 18q21.3. The invention provides methods to
 CC identify ligands that bind to MC4 receptor.
 XX Sequence 332 AA;
 SQ Query Match 5.0%; Score 7; DB 19; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 52 VLPQTGA 58
 DB 228 VLPQTGA 234

RESULT 29
 AAY17866
 ID AAY17866 standard; Protein; 332 AA.
 XX AAY17866;
 XX 17-AUG-1999 (first entry)

XX Sulfolobus solfataricus endo-beta-1,4-glucanase CelB.
 XX Sulfolobus solfataricus; endoglucanase; CelA; CelB;
 KW endo-beta-1,4-glucanase.
 OS Sulfolobus solfataricus.

FH Key Location/Qualifiers
 FT Peptide 1..21 /label= signal
 FT Protein 22..332 /label= CelB

XX DK9900097-A.
 XX 12-JAN-1999.
 XX 12-JAN-1999; 99DK-0000097.
 XX 12-JAN-1999; 99DK-0000097.
 XX (NOVO) NOVO-NORDISK AS.
 XX WPI; 1999-279376/24.
 DR N-PSDB; AAX80188.

XX Novel endonuclease - produced by Sulfolobus solfataricus
 XX Claim 1; Page 31-32; 36pp; English.

XX The present sequence represents a Sulfolobus solfataricus endoglucanase,
 CC specifically endo-beta-1,4-glucanase, designated CelB. The new
 CC endo-beta-1,4-glucanase is produced by Sulfolobus solfataricus
 CC ATCC 35092.

XX SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 20; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 STSTTTN 9
 DB 45 STSTTTN 51
 |||||

RESULT 30
 AAW87869
 ID AAW87869 standard; Protein; 332 AA.
 AC AAW87869;
 DT 26-APR-1999 (first entry)
 DE Human melanocortin receptor MC4-R.
 KW Melanocortin receptor; MC4-R; human; acne; therapy;
 KW G-protein coupled receptor.
 XX Homo sapiens.
 OS
 XX WO9856914-A1.
 XX PD 17-DEC-1998.
 XX PF 12-JUN-1998; 98WO-US12098.
 XX PR 13-JUN-1997; 97US-0050063.
 XX PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX PI Chen W, Cone RD, Low MJ;
 XX DR WPI; 1999-080902/07.
 XX DR N-PSDB; AAV63707.
 XX PT Identifying compounds that bind to melanocortin receptors - such as
 XX therapeutic agents for treating exocrine disorders like acne
 XX Example 2F; Page 71-73; 14pp; English.

XX This is the amino acid sequence of human melanocortin receptor
 CC MC4-R, as deduced from the nucleotide sequence of an isolated
 CC genomic DNA clone (see AAV63707). MC4-R is a G-protein coupled
 CC receptor. The invention relates to the cloning, expression and
 CC functional characterisation of mammalian melanocortin receptor
 CC MC1-R, MC2-R, MC3-R, MC4-R and MC5-R nucleic acids (see AAV63702-08)
 CC and polypeptides (see AAW87864-70), as well as expression constructs,
 CC eukaryotic cells transformed with such constructs, knockout
 CC animals, and methods and reagents for developing agonists and
 CC antagonists specific for mammalian melanocortin receptors. Such
 CC compounds, particularly those specific for MC5-R, are used to treat
 CC disorders of exocrine gland function, e.g. of the lacrimal or
 CC sebaceous glands, particularly acne, other skin disorders and 'dry
 CC eye', also disorders related to oestrus, mating, gestation and
 CC other pheromone-related conditions.

XX SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 20; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 DB 228 VLPGTGA 234
 |||||

RESULT 32
 AAB18769
 ID AAB18769 standard; Protein; 332 AA.
 AC AAB18769;
 DT 22-JAN-2001 (first entry)
 DE A human melanocortin-4 receptor polypeptide.
 KW Human; melanocortin-1 receptor; melanocortin-2 receptor; 16q24.3;
 KW 18p11.2; melanocortin-3 receptor; 20q13.2; melanocortin-4 receptor;
 KW 18q21.3; melanocortin.

RESULT 31
 AAW92442
 ID AAW92442 standard; Protein; 332 AA.
 XX AC AAW92442;
 XX DT 21-APR-1999 (first entry)
 XX DE Human MC4 protein.
 XX KW Melanocortin-4 receptor; MC1; MC2; MC3; MC4; MC5; detection; probe;
 XX receptor binding; secondary signalling; tissue distribution.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Protein 1..332
 FT /note= "No stop codon given"
 XX PN US5869257-A.
 XX PD 09-FEB-1999.
 XX PF 23-APR-1997; 97US-0842238.
 XX PR 17-FEB-1994; 94US-0200711.
 XX PR 27-JUN-1996; 96US-0671525.
 XX PR 23-APR-1997; 97US-0842238.
 XX PA (UNMI) UNIV MICHIGAN.
 XX PI Gantz I, Yamada T;
 XX DR WPI; 1999-152760/13.
 XX DR N-PSDB; AAX01964.
 XX PT Probe for detecting melanocortin-4 receptor genes - that
 XX specifically hybridises to defined DNA sequence
 XX Example 1; Column 45-46; 60pp; English.

XX This sequence represents the human melanocortin-4 receptor, MC4. This
 CC protein is used in a method in which a nucleic acid probe useful for
 CC specifically detecting melanocortin-4 receptor genes is described.
 CC This probe is used to isolate genes encoding melanocortin receptors,
 CC to characterise melanocortin receptor binding and secondary signalling
 CC and to determine tissue distribution of the melanocortin receptors.

XX SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 20; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 DB 228 VLPGTGA 234
 |||||

RESULT 32
 AAB18769
 ID AAB18769 standard; Protein; 332 AA.
 AC AAB18769;
 DT 22-JAN-2001 (first entry)
 DE A human melanocortin-4 receptor polypeptide.
 KW Human; melanocortin-1 receptor; melanocortin-2 receptor; 16q24.3;
 KW 18p11.2; melanocortin-3 receptor; 20q13.2; melanocortin-4 receptor;
 KW 18q21.3; melanocortin.

XX OS Homo sapiens.
XX US6117975-A.
XX PD 12-SEP-2000.
XX PF 23-JUL-1996; 96US-0629335.
XX PR 17-FEB-1994; 94US-0200711.
XX PA (UNMI) UNIV MICHIGAN.
XX PI Gantz I, Yamada T;
XX DR WPI; 2000-610853/58.
XX DR N-PSDB; AAA75829.
XX PT New melanocortin receptor polypeptides MC3 and MC4, and genes encoding
PT the receptors, useful for providing therapeutic vehicles employed in
PT treating disorders involving melanocortin receptor function -
XX Claim 5; Column 45-48; 59pp; English.
XX CC The present sequence represents human melanocortin receptor polypeptide.
CC Melanocortin-1 and melanocortin-2 receptor genes have been localised to
CC Chromosome 16q24.3 and 18p11.2, respectively. The melanocortin-3 receptor
CC gene has been localised to chromosome loci 20q13.2-q13.3. The
CC melanocortin-4 receptor has been localised to chromosome 18q21.3. The
CC sequence of melanocortin-3 receptor is activated primarily by the core heptapeptide
CC sequence of melanocortins, with an adjacent terminal tyrosine being
CC required for full activation. The melanocortin receptors and their
CC respective genes are useful in providing therapeutic vehicles for the
CC treatment of processes involving the function of melanocortin receptors.
CC The genes encoding the melanocortin receptors are useful for transfecting
CC mammalian cells lacking endogenous melanocortin receptors to induce
CC expression.
XX SQ Sequence 332 AA;
Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VLPGTGA 58
Db 228 VLPGTGA 234
RESULT 33
AAB02845
XX ID AAB02845 standard; Protein; 332 AA.
XX AC AAB02845;
XX DT 22-AUG-2000 (first entry)
XX DE Human G protein coupled receptor MC4 protein SEQ ID NO:74.
XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.
XX OS Homo sapiens.
XX FN WO200022131-A2.
XX PD 20-APR-2000.
XX PF 13-OCT-1999; 99WO-US24065.
XX PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.

PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156655.
PR 29-SEP-1999; 99US-0156634.
XX PA (AREN-) ARENA PHARM INC.
XX PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX DR WPI; 2000-317986/27.
XX DR N-PSDB; AAA46069.
XX PT Non-endogenous, human G protein-coupled receptors for screening
XX receptor, inverse or partial agonists useful as therapeutic agents -
XX Example 1; Page 133-134; 187pp; English.
XX CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
XX the exemplification of the present invention.
XX SQ Sequence 332 AA;
Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VLPGTGA 58
Db 228 VLPGTGA 234
RESULT 34
AAB02857
XX ID AAB02857 standard; Protein; 332 AA.
XX AC AAB02857;
XX DT 22-AUG-2000 (first entry)
XX DE Human G protein coupled receptor hMC4 (A244K) protein SEQ ID NO:136.
XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.
XX OS Homo sapiens.
OS Synthetic.

```

2Y      52  VLPGTGA  58
        |||||
Db      228 VLPGTGA  234

RESULT 35
AAAY94301
XX      ID  AAY94301 standard; Protein; 332 AA.
AC
XX      AC  AAY94301;
XX
XX      DT  04-AUG-2000 (first entry)

```

QY 52 VLPGTGA 58
|||||
Db 228 VLPGTGA 234

RESULT 36
AAV83182
ID AAY83182 standard; protein; 332 AA.
XX
AC AAY83182;
XX
DT 24-JUL-2000 (first entry)
XX
DE Melanocortin receptor MC4 comprising Factor Xa cleavage site.
XX
XX Membrane polypeptide; lipid matrix; synthesis; ligation;
KW chemoselective ligation; fluorescence resonance energy transfer;
KW FRET; chromophore; ligand; receptor domain; drug screening;

diagnosis; ion channel; melanocortin receptor; MC4.
Synthetic.
Homo sapiens.
WO200012536-A2.
09-MAR-2000.
26-AUG-1999; 99WO-US19542.
31-AUG-1998; 98US-0144964.
05-MAR-1999; 99US-0263971.
(GRYP-) GRYPHON SCI.
Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;
WPI; 2000-270792/23.
Selectively labeled membrane peptides, useful e.g. for detecting ligand binding to receptors and in drug screening, are prepared, in lipid matrix, by reaction between amino acid residues
Example 11; Page 68-69; 120pp; English.
New methods are described by which membrane polypeptides can be labelled. The method comprises chemoselective chemical ligation of the membrane polypeptide which is incorporated in a lipid matrix, and a ligation label. Both contain an amino acid having an unprotected reactive group that together undergo chemoselective ligation to form a covalent bond. The method can be used to label folded polypeptides embedded in a lipid membrane, by treating the amino acid with an unprotected reactive group and then ligating the cleaved polypeptide with the ligation label. The ligation label can be a chromophore, thus ligand binding to membrane bound polypeptides can be detected by contacting a membrane bound polypeptide comprising a chromophore, with the ligand under investigation and screening for binding in an assay characterized by detecting fluorescence resonance energy transfer (FRET) between the chromophore and a second chromophore, the chromophores comprising a donor and acceptor pair of a resonance energy transfer system. The methods are used for lipid matrix-assisted chemical ligation and synthesis of membrane polypeptides. Labeled membrane polypeptides are used to detect ligand binding and the identification of receptor domains, e.g. for structure/activity studies. They can also be used in drug screening, selection or design, and for diagnosis. The methods are particularly used for fluorescent resonance energy transfer (FRET) analysis of site-specific incorporation of labels during polypeptide synthesis and analysis of previously inaccessible membrane proteins. This sequence is the sequence of Melanocortin receptor MC4 which also comprises a Factor Xa cleavage site. Cleavage with Factor Xa gives a C-terminal alpha-thioester modified MC4 receptor ligation label (AA83183) and an MC4 receptor membrane polypeptide cleavage product (AA83184). Chemical ligation of cleaved MC4 in alternative membrane patches or micelles to an MC4 ligation label produces the synthetic labeled MC4 product (AA83185).

AA83185 standard; peptide; 332 AA.
AA83185;
24-JUL-2000 (first entry)
Synthetic labeled melanocortin receptor MC4.
Membrane polypeptide; lipid matrix; synthesis; ligation; chemoselective ligation; fluorescence resonance energy transfer; FRET; chromophore; ligand; receptor domain; drug screening; diagnosis; ion channel; melanocortin receptor; MC4.
Synthetic.
Homo sapiens.
WO200012536-A2.
09-MAR-2000.
26-AUG-1999; 99WO-US19542.
31-AUG-1998; 98US-0144964.
05-MAR-1999; 99US-0263971.
(GRYP-) GRYPHON SCI.
Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;
WPI; 2000-270792/23.
Selectively labeled membrane peptides, useful e.g. for detecting ligand binding to receptors and in drug screening, are prepared, in lipid matrix, by reaction between amino acid residues
Example 11; Page 71; 120pp; English.
New methods are described by which membrane polypeptides can be labelled. The method comprises chemoselective chemical ligation of the membrane polypeptide which is incorporated in a lipid matrix, and a ligation label. Both contain an amino acid having an unprotected reactive group that together undergo chemoselective ligation to form a covalent bond. The method can be used to label folded polypeptides embedded in a lipid membrane, by treating the amino acid with an unprotected reactive group and then ligating the cleaved polypeptide with the ligation label. The ligation label can be a chromophore, thus ligand binding to membrane bound polypeptides can be detected by contacting a membrane bound polypeptide comprising a chromophore, with the ligand under investigation and screening for binding in an assay characterized by detecting fluorescence resonance energy transfer (FRET) between the chromophore and a second chromophore, the chromophores comprising a donor and acceptor pair of a resonance energy transfer system. The methods are used for lipid matrix-assisted chemical ligation and synthesis of membrane polypeptides. Labeled membrane polypeptides are used to detect ligand binding and the identification of receptor domains, e.g. for structure/activity studies. They can also be used in drug screening, selection or design, and for diagnosis. The methods are particularly used for fluorescent resonance energy transfer (FRET) analysis of site-specific incorporation of labels during polypeptide synthesis and analysis of previously inaccessible membrane proteins. A C-terminal alpha-thioester modified MC4 receptor ligation label (AA83183) can be cleaved with Factor Xa to give a C-terminal alpha-thioester modified MC4 receptor ligation label (AA83184) and an MC4 receptor membrane polypeptide cleavage product (AA83185). Chemical ligation of cleaved MC4 in alternative membrane patches or micelles to an MC4 ligation label produces this synthetic labeled MC4 product (AA83185).

RESULT 37
AA83185

Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VLPGTGA 58
|||||
Db 228 VLPGTGA 234

Query Match 5.0%; Score 7; DB 21; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 52 VLPGTGA 58
 228 VLPGTGA 234

RESULT 38
 AAY87415
 ID AAY87415 standard; protein; 332 AA.
 AC AAY87415;
 CC
 CT 03-JUL-2000 (first entry)
 CW Melanocortin-4 receptor (MC4-R).
 CX Melanocortin-4 receptor; MC4-R; inhibitor; addictive behaviour;
 CY drug addiction; cocaine; morphine; obsessive-compulsive disorder.
 CZ Mammalia.
 CS
 CX WO200014115-A1.
 CY 16-MAR-2000.
 CZ 30-AUG-1999; 99WO-US19790.
 CX 03-SEP-1998; 98US-0099104.
 CY (MILL-) MILLENNIUM PHARM INC.
 CZ Duman R;
 CX
 CY WPI; 2000-256944/22.
 CZ
 CX Identification of compounds that regulate addictive behavior for
 treatment of addictive behavior disorders, such as obsessive-compulsive
 disease, comprises determining whether compounds are antagonists to
 melanocortin-4 receptor -

Claim 1; Fig 1; 62pp; English.

The invention relates to methods for the identification of compounds that regulate addictive behaviour, particularly drug addiction. The method comprises determining whether a test compound can bind to and antagonise a melanocortin-4 receptor (MC4-R), and administering that compound to an animal in order to see if a reduction in addictive behaviour occurs. Melanocortins are products of pro-opiomelanocortin post-translational processing which are thought to have a broad range of physiological actions, including behaviour, learning, memory, analgesia, thermoregulation and body weight, as well as their well known effects on adrenal cortical functions and on melanocytes. The present invention is based on the observations that MC4-R activity potentiates some of the addictive effects of drugs of addiction, particularly cocaine and morphine, and that knockout mice do not display the behavioural responses indicative of addiction caused by chronic and/or acute administration of these drugs. The methods are useful for identifying MC4-R inhibitors. These compounds may be used to treat addiction to a wide variety of substances, including cocaine, opiates, alcohol, hallucinogens, minor tranquilisers, nicotine and stimulants. The methods are also useful for the treatment of addictive behaviour disorders, including extreme craving, addictive psychological disease or obsessive-compulsive disorder. The present sequence represents a mammalian MC4-R.

Sequence 332 AA;

Query Match 5.0%; Score 7; DB 21; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 DB 228 VLPGTGA 234

RESULT 39
 AAB68490
 ID AAB68490 standard; Protein; 332 AA.
 XX
 AC AAB68490;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Amino acid sequence of a human melanocortin-4 receptor (MC-R4).
 XX
 KW Human; melanocortin-4 receptor; MC-R4; transgenic animal; body weight; food intake; obesity; diabetes; anorexia; cachexia; cancer;
 KW sexual dysfunction; pain; impaired memory; neuronal regeneration;
 KW neuropathy; growth disorder; growth hormone;
 KW insulin-like growth factor-1.
 XX
 OS Homo sapiens.
 XX
 PN WO200133956-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 13-NOV-2000; 2000WO-US31061.
 XX
 PR 12-NOV-1999; 99US-0165074.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Van Der Ploeg LHT, Chen AS, Chen HY, Forrest MJ, MacIntyre DB;
 PI Metzger JM, Palyha OC, Feighner SD, Hreniuk D;
 XX
 DR WPI; 2001-343541/36.
 DR N-PSDB; AAF85465.
 XX
 PT New transgenic animal with non-functional gene for melanocortin-4 receptor, useful for identifying specific modulators, potentially used for treating obesity or diabetes -

Disclosure; Fig 2; 58pp; English.

The present sequence represents a human melanocortin-4 receptor (MC-R4). The specification describes transgenic non-human animals whose somatic and germ cells contain at least one non-functional gene for MC-4R protein. The transgenic animals, or cells derived from them, are used to screen for compounds that modulate MC-4R. These modulators are potentially useful for regulating body weight and food intake and treatment of associated diseases, obesity; diabetes; anorexia; cachexia; cancer; sexual dysfunction; pain; impaired memory or neuronal regeneration; neuropathy; growth disorders linked to growth hormone and insulin-like growth factor-1. They can also be used to study MC-4R expression and activity.

XX Sequence 332 AA;

Query Match 5.0%; Score 7; DB 22; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 DB 228 VLPGTGA 234

RESULT 40
 AAE15746
 ID AAE15746 standard; Protein; 332 AA.
 XX
 AC AAE15746;

Search completed: November 14, 2003, 10:50:35
Job time : 55 secs

XX 26-MAR-2002 (first entry)
DT Human melanocortin 4-receptor (MC4R).
XX
XX
XX Human melanocortin 4-receptor (MC4R).
XX
XX Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
KW MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
KW ASO; gene therapy; anorectic; chromosome 18q22.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 103
FT /note= "Ile at this position is replaced with Val
FT due to single nucleotide polymorphism"
FT
FT Misc-difference 176
FT /note= "Ala at this position is replaced with Val
FT due to single nucleotide polymorphism"
FT
FT Misc-difference 202
FT /note= "Phe at this position is replaced with Leu
FT due to single nucleotide polymorphism"
FT
FT Misc-difference 251
FT /note= "Ile at this position is replaced with Leu
FT due to single nucleotide polymorphism"
XX
XX WO200179222-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 12-APR-2001; 2001WO-US11943.
PF
XX
XX 12-APR-2000; 2000US-196677P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Bentivegna SC, Choi JY, Kazemi A, Lee HH, Nandabalan K, Parks KE;
PI Sausker EA;
PI
XX WPI; 2002-082744/11.
DR N-PSDB; AAD25896, AAD25897.
DR
XX Novel polymorphic variants of melanocortin 4-receptor gene useful in
PT studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases related to the protein activity e.g.
PT obesity -
XX
XX Claim 27; Fig 3; 53pp; English.
PS
XX The invention relates to single nucleotide polymorphisms (SNP) in human
CC melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful
CC for improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated
CC with MC4R activity, e.g. obesity. MC4R gene is useful in studying the
CC expression and function of MC4R and in expressing MC4R protein for
CC use in screening for candidate drugs to treat diseases related to
CC MC4R activity and in studying the effect of the variation on the
CC biological activity of MC4R as well as on the binding affinity of
CC candidate drugs targeting MC4R for the treatment of obesity. MC4R
CC antibody is useful in a variety of diagnostic and prognostic formats
CC and in therapeutic methods. Allele-specific oligonucleotide (ASO) is
CC useful as probes and primers, and for assaying a polymorphism in
CC MC4R gene. MC4R DNA is used in gene therapy. The present sequence is
CC human MC4R protein. MC4R gene is located on chromosome 18q22.
XX
XX Sequence 332 AA;
SQ

Query Match 5.0%; Score 7; DB 23; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 52 VLPGTGA 58
Db 228 VLPGTGA 234

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:49:31 ; Search time 43 Seconds

(without alignments)
138,740 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 141

Sequence: 1 MESSTTTFVAENRPTFGE.....RAEYFRLHLSLKSGVNRLLI 141

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

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- 3: /cgn2_6/prodata/1/aaa/6A-COMB.pep:*
- 4: /cgn2_6/prodata/1/aaa/6B-COMB.pep:*
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- 6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	7	5.0	332	1	US-08-672-109B-8
7	7	5.0	332	2	US-08-842-045-8
8	7	5.0	332	2	US-08-842-238-8
9	7	5.0	332	2	US-08-662-560-2
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ALIGNMENTS

RESULT 1
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; Sequence 42, Application US/09230041A
; Patent No. 6465179
; GENERAL INFORMATION:
; APPLICANT: THIREOS, GEORGE
; APPLICANT: KAPETZOPOULOS, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/09/230,041A
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: EP97108240.9
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-09-230-041-42

Query Match 5.0%; Score 7; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 SAIAATV 65
Db 10 SAIAATV 16
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RESULT 2
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; Patent No. 6465179
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; APPLICANT: KAPETZOPOULOS, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/09/230,041A
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: EP97108240.9
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-09-230-041-37

Query Match 5.0%; Score 7; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 SAIAATV 65
Db 10 SAIAATV 16
|||||

RESULT 3
US-09-384-302A-8
; Sequence 8, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE REFERENCE: gfrn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-384-302A-8

Query Match 5.0%; Score 7; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 189 VLPGTGA 195
|||||

RESULT 4
US-09-325-932A-190
; Sequence 190, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-190

```

Query Match      5.0%; Score 7; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 FRHLRSL 132
Db 252 FRHLRSL 258
|||||

RESULT 5
US-08-671-525B-8
; Sequence 8, Application US/08671525B
; Patent No. 5703220
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,525B
; FILING DATE: June 27, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION/DOCKET NUMBER: 2115-000853DVB
; REFERENCE/DOCKET NUMBER: 2115-000853DVB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-671-525B-8

Query Match      5.0%; Score 7; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234
|||||

RESULT 6
US-08-672-109B-8
; Sequence 8, Application US/08672109B
; Patent No. 570265
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,045
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION/DOCKET NUMBER: 2115-000853DVE
; REFERENCE/DOCKET NUMBER: 2115-000853DVE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-109B-8

Query Match      5.0%; Score 7; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234
|||||

RESULT 7
US-08-842-045-8
; Sequence 8, Application US/08842045
; Patent No. 5817787
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,045
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION/DOCKET NUMBER: 2115-000853DVE
; REFERENCE/DOCKET NUMBER: 2115-000853DVE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-109B-8

```

US-08-842-045-8

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
| | | | |
DB 228 VLPGTGA 234

RESULT 8

US-08-842-238-8
; Sequence 8, Application US/08842238
; Patent No. 5869257
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ica
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS: 23
; ADDRESSEE: Hainess, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842.238
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-842-238-8

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
| | | | |
DB 228 VLPGTGA 234

RESULT 9

US-08-662-560-2
; Sequence 2, Application US/08662560
; Patent No. 5908609
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Wei, Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,560
FILING DATE: 10-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-060
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-662-560-2

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
| | | | |
DB 228 VLPGTGA 234

RESULT 10

US-08-780-749A-2
; Sequence 2, Application US/08780749A
; Patent No. 5932779
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,749A
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Laura A. Coruzzi

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-064
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-780-749A-2

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 11
US-08-780-749A-6
Sequence 6, Application US/08780749A
Patent No. 5932779
GENERAL INFORMATION:
APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,749A
FILING DATE: 08-JAN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-064
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-780-749A-6

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58

us-10-08/-5/3-2.01190.fai

DB 228 VLPGTGA 234

RESULT 12
US-08-706-281A-16
Sequence 16, Application US/08706281A
Patent No. 6100048
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Fan, Wei
APPLICANT: Kesterton, Robert A
APPLICANT: Lu, Dongsi
APPLICANT: Chen, Wenbiao
TITLE OF INVENTION: Methods and Reagents for Discovering and
TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagonist
TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-281A-16

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 13
US-08-629-335B-8
Sequence 8, Application US/08629335B
Patent No. 6117975
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills

STATE: MI
COUNTRY: US
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/629,335B
APPLICATION NUMBER: US/08/629,335B
FILING DATE: July 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-000853DBA
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-629-335B-8

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 14
US-09-097-231-16
Sequence 16, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
Low, Malcolm J
Chen, Wenbiao
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,231
FILING DATE: 12-Jun-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-097-231-16

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 15
US-08-870-511-2
Sequence 2, Application US/08870511
Patent No. 6287763
GENERAL INFORMATION:
APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
FILE REFERENCE: 7853-083
CURRENT APPLICATION NUMBER: US/08/870,511
CURRENT FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
US-08-870-511-2

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 16
US-08-870-511-6
Sequence 6, Application US/08870511
Patent No. 6287763
GENERAL INFORMATION:
APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
FILE REFERENCE: 7853-083
CURRENT APPLICATION NUMBER: US/08/870,511
CURRENT FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
US-08-870-511-6

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 17
US-08-870-511-8
; Sequence 8, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-8

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 18
US-08-870-511-10
; Sequence 10, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-10

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 19
US-08-870-511-12
; Sequence 12, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083

; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-12

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 20
US-09-384-302A-6
; Sequence 6, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; TITLE OF INVENTION: of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-384-302A-6

Query Match 5.0%; Score 7; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 21
US-09-384-302A-9
; Sequence 9, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; TITLE OF INVENTION: of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964

PRIOR FILING DATE: 1998-08-31
 PRIOR APPLICATION NUMBER: 09/263,971
 PRIOR FILING DATE: 1999-03-05
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 9
 LENGTH: 332
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-384-302A-9

Query Match 5.0%; Score 7; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 |||||
 Db 228 VLPGTGA 234

RESULT 22
 US-09-353-099-16
 Sequence 16, Application US/09353099
 Patent No. 6476187
 GENERAL INFORMATION:
 APPLICANT: Cone, Roger D
 Fan, Wei
 Boston, Bruce A
 Kesterton, Robert A
 Lu, Dongxi
 Chen, Wenbiao

TITLE OF INVENTION: Methods and Reagents for Discovering and Using Mammalian Melanocortin Receptor Agonists and Antagonists To Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 STREET: 300 South Wacker Drive
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/353,099
 FILING DATE: 14-Sep-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/706,281
 FILING DATE: 04-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6476187ran, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 96,886
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-913-0001
 TELEFAX: 312-913-0002
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 332 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-353-099-16

Query Match 5.0%; Score 7; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 |||||
 Db 228 VLPGTGA 234

RESULT 23
 US-09-831-206-2
 Sequence 2, Application US/09831206
 Patent No. 6573070
 GENERAL INFORMATION:
 APPLICANT: MacNeil, Douglas J.
 APPLICANT: Weinberg, David H.
 APPLICANT: Van der Ploeg, Leonardus H. T.
 TITLE OF INVENTION: DNA MOLECULES ENCODING THE MELANOCORTIN
 RECEPTOR PROTEIN FROM RHESUS MONKEY
 FILE REFERENCE: 20190P
 CURRENT APPLICATION NUMBER: US/09/831,206
 CURRENT FILING DATE: 2001-06-28
 PRIOR APPLICATION NUMBER: PCT/US99/25767
 PRIOR FILING DATE: 1999-11-05
 PRIOR APPLICATION NUMBER: 60/107,721
 PRIOR FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 332
 TYPE: PRT
 ORGANISM: rhesus monkey (Macaca mulatta)
 US-09-831-206-2

Query Match 5.0%; Score 7; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 |||||
 Db 228 VLPGTGA 234

RESULT 24
 US-09-252-991A-29610
 Sequence 29610, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 29610
 LENGTH: 341
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-29610

Query Match 5.0%; Score 7; DB 4; Length 341;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERLAMLR 42
 |||||
 Db 90 ERLAMLR 96

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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6840

Query Match      5.0%; Score 7; DB 4; Length 522;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      211 GTGASAI 217

RESULT 28
US-09-328-352-6683
; Sequence 6683, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6683
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6683

Query Match      5.0%; Score 7; DB 4; Length 525;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      201 GTGASAI 207

RESULT 29
US-09-252-991A-23068
; Sequence 23068, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23068
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23068

Query Match      5.0%; Score 7; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      209 GTGASAI 215

RESULT 30
US-08-268-251-19
```

```

; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6840

Query Match      5.0%; Score 7; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      202 GTGASAI 208

RESULT 27
US-09-328-352-6840
; Sequence 6840, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6840
; LENGTH: 522
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```

; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6474

Query Match      5.0%; Score 7; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      36 ERLAMLR 42
Db      327 ERLAMLR 333

RESULT 26
US-09-328-352-6474
; Sequence 6474, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6474
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6474

Query Match      5.0%; Score 7; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      202 GTGASAI 208

RESULT 27
US-09-328-352-6840
; Sequence 6840, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6840
; LENGTH: 522
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```

; Sequence 19, Application US/08268251
; Patent No. 5585475
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,251
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,219
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 272.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-268-251-19

Query Match 4.3%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 LRSLSK 134
Db 7 LRSLSK 12

RESULT 31
PCT-US93-01112-19
; Sequence 19, Application PC/TUS9301112
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01112
; FILING DATE: 19930208
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 07/831,219
; APPLICATION NUMBER:
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 272.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-01112-19

Query Match 4.3%; Score 6; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 LRSLSK 134
Db 7 LRSLSK 12

RESULT 32
US-09-205-258-1217
; Sequence 1217, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1217
; TYPE: PRT
; LENGTH: 20
; ORGANISM: Homo sapiens
; US-09-205-258-1217

Query Match 4.3%; Score 6; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 LKSGQV 137
DB 1 LKSGQV 6
|||||

RESULT 33
US-08-268-251-49
; Sequence 49, Application US/08268251
; Patent No. 5585475
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R

Query Match 4.3%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LRSLSK 134
DB 9 LRSLSK 14
|||||

RESULT 34
PCT-US93-01112-49
; Sequence 49, Application PC/TUS9301112
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01112
; FILING DATE: 19930208
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 272.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2706
TELEFAX: (510) 658-3542
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-01112-49

Query Match 4.3%; Score 6; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LRLSKS 134
Db 9 LRLSKS 14

RESULT 35
US-08-658-136-38
Sequence 38, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: OLAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-658-136-38

Query Match 4.3%; Score 6; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 127 RHLRSL 132
Db 2 RHLRSL 7

RESULT 36
US-08-179-632-8
Sequence 8, Application US/08179632
Patent No. 5607914
GENERAL INFORMATION:
APPLICANT: Rao, A. Gururaj; Zhong, Lingxiu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/Microsoft Windows
SOFTWARE: Microsoft Windows No. 5607914epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,632
FILING DATE: 07-JAN-1994
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/079,512
FILING DATE: 06/18/93
ATTORNEY/AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0233 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 245-3594
TELEFAX: (515) 245-3634
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-179-632-8

Query Match 4.3%; Score 6; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 LRALAG 46
Db 21 LRALAG 26

RESULT 37
US-08-440-174A-8
Sequence 8, Application US/08440174A
Patent No. 5717061
GENERAL INFORMATION:
APPLICANT: Rao, Gururaj A.
APPLICANT: Zhong, Lingxiu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: 7100 N.W. 62nd Avenue
CITY: Johnston

STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,174A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,512
FILING DATE: 18-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bobrowicz, Donna
REGISTRATION NUMBER: 32,196
REFERENCE/DOCKET NUMBER: 0234R2D-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4896
TELEFAX: (515) 334-6883
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-174A-8

Query Match 4.3%; Score 6; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 41 LRALAG 46
Db 21 LRALAG 26

RESULT 38
PCT-US95-00062-8
; Sequence 8, Application PC/TUS9500062
; GENERAL INFORMATION:
; APPLICANT: Pioneer Hi-Bred International, Inc.
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/Microsoft Windows
; SOFTWARE: Microsoft Windows Notepad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00062
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.; Sweeney, Patricia A.;
; NAME: Roth, Michael J.; & Simon, Soma G.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 234R2-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800

TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00062-8

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Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

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Db 21 LRALAG 26

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; Sequence 1215, Application US/09205258
; Patent No. 8525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
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; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
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; EARLIER APPLICATION NUMBER: 60/048,895
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; EARLIER FILING DATE: 1997-06-06

Fri Nov 21 10:37:37 2003

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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1215
LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1215

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Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 LKSGV 137
Db 15 LKSGV 20

RESULT 40
US-09-134-001C-2886
Sequence 2886, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2886
LENGTH: 63
TYPE: PRT
ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2886

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Db 35 LPGTGA 40

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Job time : 52 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:52:17 ; Search time 30 Seconds
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858.030 Million cell updates/sec

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Perfect score: 141
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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	7	5.0	16	15	US-10-225-567A-1062
5	7	5.0	32	12	US-10-179-382-42
6	7	5.0	35	12	US-10-179-382-37
7	7	5.0	320	15	US-10-219-220-190
8	7	5.0	332	12	US-10-318-661-27
9	7	5.0	332	12	US-10-373-355-2
10	7	5.0	332	12	US-10-413-752-2
11	7	5.0	332	12	US-10-413-752-6
12	7	5.0	332	15	US-10-288-160-16
13	7	5.0	332	15	US-10-074-754-2
14	7	5.0	332	15	US-10-225-567A-158
15	7	5.0	338	9	US-09-815-242-11881

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Sequence 3468, Ap
Sequence 10278, A
Sequence 8468, Ap
Sequence 11059, A
Sequence 211, App
Sequence 135, App
Sequence 63, Appl
Sequence 305, App
Sequence 340, App
Sequence 292, App
Sequence 327, App
Sequence 339, App
Sequence 326, App
Sequence 13, Appl
Sequence 1217, Ap
Sequence 1217, Ap
Sequence 33, Appl
Sequence 303, App
Sequence 290, App
Sequence 302, App
Sequence 289, App
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Sequence 1716, Ap
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Sequence 411, App
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Sequence 12548, A

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ALIGNMENTS

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; Sequence 2, Application US/10087573
; Publication No. US20030165872A1
; GENERAL INFORMATION:
; APPLICANT: SCHEITERS, Theodorius PM
; APPLICANT: CARCY, Bernard PD
; APPLICANT: DRACULOVSKI, Pascal R
; APPLICANT: GORENFLOT, Andre F
; TITLE OF INVENTION: BABESIA CANIS VACINE
; FILE REFERENCE: SCHEITERS
; CURRENT APPLICATION NUMBER: US/10/087,573
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: EP 01200816.5
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Babesia canis
US-10-087-573-2
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; Publication No. US20030165872A1
; GENERAL INFORMATION:
; APPLICANT: SCHEITERS, Theodorius PM
; APPLICANT: CARCY, Bernard PD
; APPLICANT: DRACULOVSKI, Pascal R
; APPLICANT: GORENFLOT, Andre F
; TITLE OF INVENTION: BABESIA CANIS VACINE
; FILE REFERENCE: SCHEITERS
; CURRENT APPLICATION NUMBER: US/10/087,573
; CURRENT FILING DATE: 2002-02-28
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; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 10
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; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11753
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
```



```
US-10-156-761-11753
Query Match      5.7%; Score 8; DB 15; Length 467;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 GTGASAI 62
Db 413 GTGASAI 420

RESULT 4
US-10-225-567A-1062
; Sequence 1062, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Butner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1062
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1062

Query Match      5.0%; Score 7; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 5 VLPGTGA 11

RESULT 5
US-10-179-382-42
; Sequence 42, Application US/10179382
; Publication No. US20030166235A1
; GENERAL INFORMATION:
; APPLICANT: THIREOS, GEORGE
; APPLICANT: KAFETZOPOULOS, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/10/179,382
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US/09/230,041
; PRIOR FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-10-179-382-42

Query Match      5.0%; Score 7; DB 12; Length 32;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 SAIAATV 65
Db 10 SAIAATV 16
```

```
RESULT 6
US-10-179-382-37
; Sequence 37, Application US/10179382
; Publication No. US20030166235A1
; GENERAL INFORMATION:
; APPLICANT: THIREOS, GEORGE
; APPLICANT: KAFETZOPOULOS, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/10/179,382
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US/09/230,041
; PRIOR FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-10-179-382-37

Query Match      5.0%; Score 7; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 SAIAATV 65
Db 10 SAIAATV 16

RESULT 7
US-10-219-220-190
; Sequence 190, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Flinn, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE REFERENCE: death and their use in the modification of plant development
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-190

Query Match      5.0%; Score 7; DB 15; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 FRHLRSL 132
Db 252 FRHLRSL 258

RESULT 8
US-10-318-661-27
; Sequence 27, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; FILE REFERENCE: Expression of A G Protein-Coupled Receptor Activated
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
```


; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,349
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-27

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 9
US-10-373-355-2
; Sequence 2, Application US/10373355
; Publication No. US20030166009A1
; GENERAL INFORMATION:
; APPLICANT: MacNeill, Douglas J.
; APPLICANT: Weinberg, David H.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: DNA MOLECULES ENCODING THE MELANOCORTIN
; TITLE OF INVENTION: 4 RECEPTOR PROTEIN FROM RHESUS MONKEY
; FILE REFERENCE: 20190P
; CURRENT APPLICATION NUMBER: US/10/373,355
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/831,206
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/US99/25767
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,721
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: rhesus monkey (Macaca mulatta)
US-10-373-355-2

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 10
US-10-413-752-2
; Sequence 2, Application US/10413752
; Publication No. US20030171295A1
; GENERAL INFORMATION:
; APPLICANT: Frank Lee
; APPLICANT: Dennis Huszar
; APPLICANT: Wei Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
; TITLE OF INVENTION: IN THE REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-145
; CURRENT APPLICATION NUMBER: US/10/413,752
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/322,695

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/662,560
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-413-752-2

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 11
US-10-413-752-6
; Sequence 6, Application US/10413752
; Publication No. US20030171295A1
; GENERAL INFORMATION:
; APPLICANT: Frank Lee
; APPLICANT: Dennis Huszar
; APPLICANT: Wei Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
; TITLE OF INVENTION: IN THE REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-145
; CURRENT APPLICATION NUMBER: US/10/413,752
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/322,695
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/662,560
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-413-752-6

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 12
US-10-288-160-16
; Sequence 16, Application US/10288160
; Publication No. US20030105024A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Fan, Wei
; APPLICANT: Boston, Bruce A
; APPLICANT: Kesterton, Robert A
; APPLICANT: Lu, Dongxi
; APPLICANT: Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; Using Mammalian Melanocortin Receptor Agonists and Antagon
; To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago

```
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/288,160
; FILING DATE: 05-NO. US20030105024A1-2002
; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20030105024A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-288-160-16

Query Match          5.0%; Score 7; DB 15; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 13
US-10-074-754-2
; Sequence 2, Application US/10074754
; Publication No. US20030113263A1
; GENERAL INFORMATION:
; APPLICANT: Marks, Daniel L.
; APPLICANT: Cone, Roger D.
; TITLE OF INVENTION: Methods and Reagents for Discovering and Using
; TITLE OF INVENTION: Mammalian Melanocortin Receptor Antagonists to Treat
; TITLE OF INVENTION: Cachexia
; FILE REFERENCE: 96-886
; CURRENT APPLICATION NUMBER: US/10/074,754
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-754-2

Query Match          5.0%; Score 7; DB 15; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 14
US-10-225-567A-158
; Sequence 158, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 158
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-158

Query Match          5.0%; Score 7; DB 15; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 15
US-09-815-242-11881
; Sequence 11881, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11881
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11881

Query Match          5.0%; Score 7; DB 9; Length 338;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 36 ERLAMLR 42
 Db 311 ERLAMLR 317

RESULT 16

US-09-866-582-10
 ; Sequence 10, Application US/09866582
 ; Patent No. US20020127620A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Witman, George B.
 ; APPLICANT: Fazour, Gregory J.
 ; APPLICANT: Rosenbaum, Joel L.
 ; APPLICANT: Cole, Douglas G.
 ; TITLE OF INVENTION: INTRACELLULAR TRANSPORT
 ; FILE REFERENCE: 07917-145001
 ; CURRENT APPLICATION NUMBER: US/09/866,582
 ; PRIOR FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: US 60/206,923
 ; PRIOR FILING DATE: 2000-05-24
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Chlamydomonas reinhardtii
 US-09-866-582-10

Query Match 5.0%; Score 7; DB 10; Length 469;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 PGTGASA 60
 Db 260 PGTGASA 266

RESULT 17

US-10-156-761-11162
 ; Sequence 11162, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 11162
 ; LENGTH: 520
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-11162

Query Match 5.0%; Score 7; DB 15; Length 520;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GTGASAI 61
 Db 193 GTGASAI 199

RESULT 18

US-10-128-714-3468
 ; Sequence 3468, Application US/10128714
 ; Publication No. US20030119013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Wenqi
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Eroshkin, Alexey M
 ; APPLICANT: Lemieux, Sebastien M
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: 10182-018-999
 ; CURRENT APPLICATION NUMBER: US/10/128,714
 ; CURRENT FILING DATE: 2002-04-23
 ; PRIOR APPLICATION NUMBER: US 60/285,697
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 8603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3468
 ; LENGTH: 699
 ; TYPE: PRT
 ; ORGANISM: Aspergillus fumigatus
 US-10-128-714-3468

Query Match 5.0%; Score 7; DB 15; Length 699;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 STKSPEL 87
 Db 336 STKSPEL 342

RESULT 19

US-09-815-242-10278
 ; Sequence 10278, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,825
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10278
 ; LENGTH: 748
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-09-815-242-10278

Query Match 5.0%; Score 7; DB 9; Length 748;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AMLRALA 45
 Db 646 AMLRALA 652

RESULT 20

; Sequence 8468, Application US/10128714
 ; Publication No. US20030119013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Wendu
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Ershkin, Alexey M
 ; APPLICANT: Lemieux, Sebastien M
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 ; FILE REFERENCE: 10182-018-999
 ; CURRENT APPLICATION NUMBER: US/10/128,714
 ; PRIOR FILING DATE: 2002-04-23
 ; PRIOR APPLICATION NUMBER: US 60/285,697
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 8603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8468
 ; LENGTH: 808
 ; TYPE: PRT
 ; ORGANISM: Aspergillus fumigatus
 US-10-128-714-8468

Query Match 5.0%; Score 7; DB 15; Length 808;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 STKSPLEL 87
 Db 445 STKSPLEL 451

RESULT 21

; Sequence 11059, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 11059
 ; LENGTH: 1029
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-11059

Query Match 5.0%; Score 7; DB 15; Length 1029;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 PGTGASA 60
 Db 92 PGTGASA 98

RESULT 22

; Sequence 211, Application US/09779308
 ; Patent No. US20020150972A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Paris
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Pia M. Challita-Eid
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Eliana Levin
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
 ; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
 ; FILE REFERENCE: 129.4USU1
 ; CURRENT APPLICATION NUMBER: US/09/779,308
 ; CURRENT FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: 60/181,020
 ; PRIOR FILING DATE: 2000-02-08
 ; NUMBER OF SEQ ID NOS: 718
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 211
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-09-779-308-211

Query Match 4.3%; Score 6; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
 Db 3 SLKSQ 8

RESULT 23

; Sequence 135, Application US/09824787B
 ; Patent No. US20020155447A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zauderer, Maurice
 ; APPLICANT: Evans, Elizabeth E.
 ; APPLICANT: Borrello, Melinda A.
 ; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
 ; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
 ; FILE REFERENCE: 1821.0040001

; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-135

Query Match 4.3%; Score 6; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 LPGTGA 58
Db 1 LPGTGA 6

RESULT 24
US-09-779-308-63
; Sequence 63, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Ava Jakobovics
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.4USUI
; CURRENT APPLICATION NUMBER: US/09/779,308
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-63

Query Match 4.3%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 4 SLKSQ 9

RESULT 25
US-10-105-232-305
; Sequence 305, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: 2002-03-26
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 305
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-305

Query Match 4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 4 SLKSQ 9

RESULT 26
US-10-105-232-340
; Sequence 340, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 340
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-340

Query Match 4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 5 SLKSQ 10

RESULT 27
US-10-189-437-292
; Sequence 292, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08

; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 292
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-292

Query Match 4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 SLKSQ 136
Db 4 SLKSQ 9

RESULT 28
US-10-189-437-327
; Sequence 327, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 327
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-327

Query Match 4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 SLKSQ 136
Db 5 SLKSQ 10

RESULT 29
US-10-105-232-339
; Sequence 339, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 339
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-339

Query Match 4.3%; Score 6; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 SLKSQ 136
Db 6 SLKSQ 11

RESULT 30
US-10-189-437-326
; Sequence 326, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 326
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-326

Query Match 4.3%; Score 6; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 SLKSQ 136
Db 6 SLKSQ 11

RESULT 31
US-09-992-665-13
; Sequence 13, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kafa Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665

```

; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-13

Query Match      4.3%; Score 6; DB 11; Length 13;
Best Local Similarity 100.0%; Pred.No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      117 PLEKRR 122
Db      4 PLEKRR 9

RESULT 32
US-09-933-767-1217
; Sequence 1217, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1217
; LENGTH: 20

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-1217

Query Match
Best Local Similarity 4.3%; Score 6; DB 12; Length 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 LKSQGV 137
Db 1 LKSQGV 6

RESULT 33
US-10-023-282-1217
; Sequence 1217, Application US/10023282
; Publication No. US2003009293A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; EARLIER FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-1217

Query Match
Best Local Similarity 4.3%; Score 6; DB 15; Length 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 LKSQGV 137
Db 1 LKSQGV 6

RESULT 34
US-10-115-072-33
; Sequence 33, Application US/10115072
; Publication No. US20030105003A1
; GENERAL INFORMATION:
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNIZATION THERAPY FOR TREATMENT OF
; TITLE OF INVENTION: ATHEROSCLEROSIS AND DEVELOPMENT OF PEPTIDE-BASED ASSAY
; TITLE OF INVENTION: FOR DETERMINATION OF IMMUNE RESPONSES AGAINST OXIDIZED
; TITLE OF INVENTION: LOW DENSITY LIPOPROTEIN
; FILE REFERENCE: 03940.0057
; CURRENT APPLICATION NUMBER: US/10/115,072
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/281,410
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0101232-7
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0103754-8
; PRIOR FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20

```


; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-115-072-33

Query Match 4.3%; Score 6; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 GASMKL 74
Db 2 GASMKL 7

RESULT 35
US-10-105-232-303
; Sequence 303, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: Patentin 2.1
; SEQ ID NO 303
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-303

Query Match 4.3%; Score 6; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 15 SLKSQ 20

RESULT 36
US-10-189-437-290
; Sequence 290, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: Patentin 2.1
; SEQ ID NO 290
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-290

Query Match 4.3%; Score 6; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 15 SLKSQ 20

RESULT 37
US-10-105-232-302
; Sequence 302, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: Patentin 2.1
; SEQ ID NO 302
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-302

Query Match 4.3%; Score 6; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 15 SLKSQ 20

RESULT 38
US-10-189-437-289
; Sequence 289, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396

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; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 289
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-289

Query Match      4.3%; Score 6; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      131 SLKSQ 136
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RESULT 39
US-09-864-761-47718
; Sequence 47718, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47718

; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006230.11
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 12
US-09-864-761-47718

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      51 RVLPGT 56
DB      12 RVLPGT 17

RESULT 40
US-10-105-232-301
; Sequence 301, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: ELEMORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 301
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-301

Query Match      4.3%; Score 6; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      131 SLKSQ 136
DB      15 SLKSQ 20

Search completed: November 14, 2003, 10:57:33
Job time : 32 secs

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M protein - protein search, using sw model

un on: November 14, 2003, 10:48:51 ; Search time 20 Seconds
(without alignments)

677.989 Million cell updates/sec

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effect score: 141

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Gapop 60.0 , Gapext 60.0

searched: 283308 seqs, 96168682 residues

ord size : 0

total number of hits satisfying chosen parameters: 283308

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aximum DB seq length: 2000000000

ost-processing: Listing first 1000 summaries

atabase :

PIR 76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	8	5.7	707	2	hypothetical prote
4	7	5.0	105	2	extensin homolog T
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6	7	5.0	154	1	hypothetical prote
7	7	5.0	215	2	mitochondrial rece
8	7	5.0	237	2	melanocortin-4 rec
9	7	5.0	238	2	transcription regu
10	7	5.0	289	2	probable flagellar
11	7	5.0	323	2	protein-export mem
12	7	5.0	330	2	probable glycosyl
13	7	5.0	332	2	melanocortin recep
14	7	5.0	332	2	endoglucanase prec
15	7	5.0	338	2	phenylalaninyl-trNA
16	7	5.0	339	2	hypothetical prote
17	7	5.0	350	2	phenylalanine-trNA
18	7	5.0	362	2	ribosomal protein
19	7	5.0	362	2	ribosomal protein
20	7	5.0	363	1	MAK32 protein - ye
21	7	5.0	378	2	membrane proteins
22	7	5.0	378	2	membrane protein h
23	7	5.0	409	2	probable PPE prote
24	7	5.0	409	2	probable PPE prote
25	7	5.0	424	1	nodulation protein
26	7	5.0	468	2	probable amidase
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28	7	5.0	491	2	probable flavin-bi
29	7	5.0	506	2	phosphoribosylamin

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31	7	5.0	527	2	A83453	probable flavin-co
32	7	5.0	538	1	T40151	histidine-trNA lig
33	7	5.0	701	1	S46458	transcription fact
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35	7	5.0	731	2	AH2546	hypothetical prote
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37	7	5.0	748	2	H85934	phosphotransferase
38	7	5.0	748	2	F65065	hypothetical prote
39	7	5.0	753	2	T32844	hypothetical prote
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41	7	5.0	841	2	T01046	hypothetical prote
42	7	5.0	860	1	EAMS	elastin precursor
43	7	5.0	864	1	EART	glycine dehydrogen
44	7	5.0	1057	2	A42109	probable pyruvate
45	7	5.0	1184	2	G71262	RAD9 protein - yea
46	7	5.0	1309	1	BVBVD9	hypothetical prote
47	7	5.0	1447	2	T15200	hypothetical prote
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49	6	4.3	34	2	PC1272	alkaline proteinas
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51	6	4.3	44	2	A84184	H-transporing tw
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53	6	4.3	62	2	F85709	hypothetical prote
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63	6	4.3	99	2	A97413	hypothetical prote
64	6	4.3	101	2	C72486	conserved hypothe
65	6	4.3	102	2	A12630	oxy upstream of m
66	6	4.3	102	2	B48360	hypothetical prote
67	6	4.3	103	2	E75071	hypothetical prote
68	6	4.3	104	2	F72369	conserved hypothe
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70	6	4.3	106	2	QJ0234	hypothetical 12.5K
71	6	4.3	107	2	QX0361	subtilisin-trypsin
72	6	4.3	111	2	T17582	hypothetical prote
73	6	4.3	111	2	S14855	hypothetical prote
74	6	4.3	116	2	G82048	probable 5-carboxy
75	6	4.3	116	2	G72520	hypothetical prote
76	6	4.3	121	2	F84868	hypothetical prote
77	6	4.3	122	2	AG0221	conserved hypothe
78	6	4.3	123	2	F82835	6-pyruvoyl tetrahy
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88	6	4.3	138	2	T49392	related to pullula
89	6	4.3	141	2	T08790	hypothetical prote
90	6	4.3	143	2	E87574	Rrf2 family protei
91	6	4.3	144	2	S01290	apolipoprotein B -
92	6	4.3	144	2	AG3178	transcription regu
93	6	4.3	145	2	B86751	prophage pi2 prote
94	6	4.3	145	2	T08435	la costa protein -
95	6	4.3	148	2	T48981	hypothetical prote
96	6	4.3	148	2	AE1811	hypothetical prote
97	6	4.3	149	1	VHBPF6	major nucleocapsid
98	6	4.3	150	2	S33784	hemoglobin VII - m
99	6	4.3	154	2	A82096	xanthine-guanine p
100	6	4.3	154	2	T34641	probable integral
101	6	4.3	157	2	S35037	helix-loop-helix p
102	6	4.3	158	2	P95051	acetylactate synth

103	6	4.3	158	2	D83382	hypothetical prote	176	4.3	232	2	S18139	dehydrin DHN3 - ga
104	6	4.3	159	2	E89861	Na+/H+ antiporter	177	4.3	232	2	B96803	hypothetical prote
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106	6	4.3	161	2	T21995	hypothetical prote	179	4.3	233	2	C90507	hypothetical prote
107	6	4.3	162	2	B71085	hypothetical prote	180	4.3	233	2	S44882	2C262.2 protein -
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110	6	4.3	165	2	D75292	conserved hypoteth	183	4.3	235	2	D48364	mucin like protein
111	6	4.3	166	2	B97922	acetolactate synth	184	4.3	235	2	C64915	dethiobiotin synth
112	6	4.3	167	2	JC5165	acetolactate synth	185	4.3	235	2	C90916	dethiobiotin synth
113	6	4.3	168	2	E70855	probable ilvN prot	186	4.3	235	2	H85764	lipocate-protein li
114	6	4.3	169	2	T45414	hypothetical prote	187	4.3	235	2	G86567	hypothetical prote
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116	6	4.3	171	2	H82799	acetyltransferase,	189	4.3	235	2	F72056	conserved hypoteth
117	6	4.3	172	2	B64094	ribosomal protein	190	4.3	236	2	E69090	hypothetical prote
118	6	4.3	173	2	C70844	probable moaC3 pro	191	4.3	236	2	A12432	hypothetical prote
119	6	4.3	174	2	S76780	hypothetical prote	192	4.3	237	2	A75400	probable phosphogl
120	6	4.3	175	2	T08444	hypothetical prote	193	4.3	237	2	T26765	hypothetical prote
121	6	4.3	176	2	E69193	conserved hypoteth	194	4.3	237	2	F97416	hypothetical prote
122	6	4.3	177	2	TPCHIS	troponin I, fast s	195	4.3	239	2	JC7768	blue fluorescent p
123	6	4.3	178	2	B83310	single-strand DNA	196	4.3	239	2	JC7768	probable manganese
124	6	4.3	179	2	A23569	troponin I, fast s	197	4.3	240	2	F90885	hypothetical prote
125	6	4.3	180	2	G83379	probable fibrial	198	4.3	240	2	C90833	hypothetical prote
126	6	4.3	181	2	TPRHIV	troponin I, slow s	199	4.3	240	2	A85733	hypothetical prote
127	6	4.3	182	2	TPRHIV	troponin I, slow s	200	4.3	240	2	B64897	hypothetical prote
128	6	4.3	183	2	B44786	troponin I, slow s	201	4.3	241	2	S19999	hypothetical prote
129	6	4.3	184	2	B85680	unknown protein en	202	4.3	241	2	F87189	conserved hypoteth
130	6	4.3	185	2	A71286	conserved hypoteth	203	4.3	241	2	F87189	outer membrane pro
131	6	4.3	186	2	T06769	probable glycogen(204	4.3	244	2	I62393	conserved hypoteth
132	6	4.3	187	2	E64942	hypothetical 21.4	205	4.3	244	2	E86523	pp-loop type ATPas
133	6	4.3	188	2	D69336	guanylate kinase I	206	4.3	245	2	T50626	hypothetical prote
134	6	4.3	189	2	D69013	conserved hypoteth	207	4.3	245	2	AB0589	hypothetical prote
135	6	4.3	190	2	S22636	hypothetical prote	208	4.3	245	2	JC6191	ATP-binding casset
136	6	4.3	191	2	T06813	dehydrin 3 - Garde	209	4.3	249	2	T48684	ribosomal protein
137	6	4.3	192	2	F83241	outer membrane lip	210	4.3	250	2	T12864	LSU ribosomal prot
138	6	4.3	193	2	E84309	hypothetical prote	211	4.3	251	2	T12864	hypothetical prote
139	6	4.3	194	2	A69429	hypothetical prote	212	4.3	251	2	S40735	probable antirepre
140	6	4.3	195	2	T42969	hypothetical prote	213	4.3	252	2	B64322	protein kinase hom
141	6	4.3	196	2	T43480	hypothetical prote	214	4.3	252	2	C69490	ribosomal protein
142	6	4.3	197	2	B83606	hypothetical prote	215	4.3	252	2	T09560	LSU ribosomal prot
143	6	4.3	198	2	AD2405	hypothetical prote	216	4.3	252	2	H72469	hypothetical prote
144	6	4.3	199	2	S52644	phycobilisome matu	217	4.3	253	2	AC1338	hypothetical prote
145	6	4.3	200	2	E83515	conserved hypoteth	218	4.3	253	2	A11708	transcription regu
146	6	4.3	201	2	T46194	hypothetical prote	219	4.3	253	2	T49820	hypothetical prote
147	6	4.3	202	2	G81336	uracil phosphoribo	220	4.3	255	2	H75147	leu ribosomal prot
148	6	4.3	203	2	S51098	probable alkyl hyd	221	4.3	255	2	G71187	probable ribosomal
149	6	4.3	204	2	E90004	uracil phosphoribo	222	4.3	255	2	T09558	hypothetical prote
150	6	4.3	205	2	C82748	stringent starvati	223	4.3	255	2	C88956	hypothetical prote
151	6	4.3	206	2	F71111	hypothetical prote	224	4.3	258	2	S25271	protein K04F1.5 [l
152	6	4.3	207	2	S77369	hypothetical prote	225	4.3	258	2	S25271	hypothetical prote
153	6	4.3	208	2	A95863	hypothetical prote	226	4.3	259	2	D84078	gene Cpi2 protein
154	6	4.3	209	2	S74055	hypothetical prote	227	4.3	260	1	D47031	p-nitrophenyl phos
155	6	4.3	210	2	H82314	conserved hypoteth	228	4.3	261	2	T45251	orf2 3' of bah - S
156	6	4.3	211	2	T36491	probable gntR-fam	229	4.3	262	2	T17442	probable cyclase h
157	6	4.3	212	2	S01358	salivary glue prot	230	4.3	265	1	G69084	ybtT protein - Yer
158	6	4.3	213	2	T15053	ribonuclease (EC 3	231	4.3	265	2	T42419	conserved hypoteth
159	6	4.3	214	2	A71711	hypothetical prote	232	4.3	265	2	T40259	hypothetical prote
160	6	4.3	215	2	A83257	hypothetical prote	233	4.3	265	2	I40868	hypothetical prote
161	6	4.3	216	2	AG0670	probable regulator	234	4.3	267	2	T47050	hypothetical prote
162	6	4.3	217	2	B69079	alkyl hydroperoxid	235	4.3	267	2	T30344	lip4 protein - Yer
163	6	4.3	218	2	G82108	amino acid ABC tra	236	4.3	267	2	AH0232	yersiniabactin bio
164	6	4.3	219	2	F68514	ABC amino acid tra	237	4.3	267	2	AI3010	hypothetical prote
165	6	4.3	220	2	G69129	hypothetical prote	238	4.3	267	2	E98273	iron(III) dicitrat
166	6	4.3	221	2	E64830	cytidylate kinase	239	4.3	269	2	A95906	hypothetical prote
167	6	4.3	222	2	G85616	cytidylate kinase	240	4.3	271	2	T51249	yjcl protein impo
168	6	4.3	223	2	AB0614	cytidylate kinase	241	4.3	274	2	I46929	stem cell factor -
169	6	4.3	224	2	G85616	cytidylate kinase	242	4.3	275	2	B81099	formamidopyrimidin
170	6	4.3	225	2	T34197	GntR family transc	243	4.3	275	2	S44961	DNA-formamidopyrim
171	6	4.3	226	2	B83629	hypothetical prote	244	4.3	275	2	AC1772	lmbN protein - Str
172	6	4.3	227	2	E89923	hypothetical prote	245	4.3	275	2	AI1396	conserved hypoteth
173	6	4.3	228	2	B82691	N-(5'-phosphoribos	246	4.3	276	2	T49220	casein kinase II (
174	6	4.3	229	2	C82141	cytidylate kinase	247	4.3	276	2	D70191	hypothetical prote
175	6	4.3	230	2	A10169	cytidylate kinase	248	4.3	279	2	S67132	hypothetical prote

249	6	4.3	280	2	G95508	protein F27F5.5 [i	322	6	4.3	331	2	D72314	ribose ABC transpo
250	6	4.3	281	2	T45926	hypothetical prote	323	6	4.3	332	2	T35917	probable regulator
251	6	4.3	281	2	E75195	hypothetical prote	324	6	4.3	332	2	T51269	hypothetical prote
252	6	4.3	281	2	H71227	hypothetical prote	325	6	4.3	333	2	AH2179	DnaJ protein [impo
253	6	4.3	281	2	AF0505	probable exported	326	6	4.3	333	2	AI0940	probable ABC trans
254	6	4.3	282	2	D87341	forminoslutamase	327	6	4.3	333	2	AI0846	hypothetical prote
255	6	4.3	282	2	E71444	homeobox protein H	328	6	4.3	336	2	G95003	membrane protein [
256	6	4.3	282	2	F64695	biotin synthetase	329	6	4.3	336	2	AI54035	transforming prote
257	6	4.3	282	2	H71822	hypothetical prote	330	6	4.3	338	1	TVMSFB	lipote-protein li
258	6	4.3	283	2	S69639	UTP-glucose-1-phos	331	6	4.3	338	2	D70382	phenylalanine-tRNA
259	6	4.3	285	2	D69184	hypothetical prote	332	6	4.3	338	2	H87510	polyprenyl synthet
260	6	4.3	285	2	C95327	hypothetical prote	333	6	4.3	338	2	DS9102	protein F25E5.2 [i
261	6	4.3	286	2	AH1038	site-specific DNA-	334	6	4.3	338	2	S73441	MG032 homolog Bol
262	6	4.3	287	2	AB2354	dihydropterolate sy	335	6	4.3	339	2	S86614	phenylalanyl tRNA
263	6	4.3	287	2	F82265	conserved hypotet	336	6	4.3	339	2	B72011	phenylalanine-tRNA
264	6	4.3	287	2	S2B371	viomycin kinase [E	337	6	4.3	339	2	AD3501	Mg(2+) chelataase f
265	6	4.3	287	2	S74050	hypothetical prote	338	6	4.3	340	2	S74768	UDPglucose 4-epime
266	6	4.3	287	2	AI2609	regulator protein	339	6	4.3	340	2	B97876	conserved hypotet
267	6	4.3	288	2	H97391	H+-transporting tw	340	6	4.3	341	2	T41286	malate dehydrogena
268	6	4.3	288	2	S73016	probable regulator	341	6	4.3	341	2	F81727	phenylalanyl-tRNA
269	6	4.3	288	2	E86717	hypothetical prote	342	6	4.3	341	2	D64221	phenylalanine-tRNA
270	6	4.3	288	2	T47614	hypothetical prote	343	6	4.3	341	2	E96019	probable sugar upt
271	6	4.3	289	2	E70984	probable drB prot	344	6	4.3	341	2	D64159	hypothetical prote
272	6	4.3	289	2	A87534	carboxylesterase f	345	6	4.3	341	2	T47653	pectate lyase-like
273	6	4.3	289	2	F97322	uncharacterized co	346	6	4.3	342	2	D71465	phenylalanine-tRNA
274	6	4.3	291	2	C87700	UTP-glucose-1-phos	347	6	4.3	342	2	T29245	hypothetical prote
275	6	4.3	292	2	T06201	xyloglucan endo-1,	348	6	4.3	342	2	S09786	hypothetical prote
276	6	4.3	292	2	E71885	hypothetical prote	349	6	4.3	343	2	A45073	hypothetical prote
277	6	4.3	292	2	A47125	transcription acti	350	6	4.3	343	2	H96654	Gai beta 1,3galNAC
278	6	4.3	293	1	WMBP11	gene 11 protein -	351	6	4.3	344	2	G81934	F16P17.15 [importe
279	6	4.3	293	1	WMBPL9	gene 11 protein -	352	6	4.3	344	2	H81171	probable dihydroor
280	6	4.3	293	2	T06232	Ps16 protein - whe	353	6	4.3	344	2	T24053	dihydroorotase NMB
281	6	4.3	294	2	E82723	hypothetical prote	354	6	4.3	345	2	T14707	hypothetical prote
282	6	4.3	294	2	T05725	cp31AHV protein -	355	6	4.3	345	2	T17608	DNA ligase homolog
283	6	4.3	295	2	AI2683	transcription regu	356	6	4.3	346	2	A99173	probable GDPmannos
284	6	4.3	297	2	H72076	hypothetical prote	357	6	4.3	346	2	AG0302	hypothetical prote
285	6	4.3	299	2	T25768	hypothetical prote	358	6	4.3	347	2	AB0509	Laci-family transc
286	6	4.3	300	2	H87631	integral membrane	359	6	4.3	347	2	T20472	[citrate (PRO-3S) -
287	6	4.3	300	2	C84732	hypothetical prote	360	6	4.3	348	2	S69719	hypothetical prote
288	6	4.3	302	2	I39495	hypothetical prote	361	6	4.3	348	2	B95970	hypothetical prote
289	6	4.3	302	2	F95990	probable transcrip	362	6	4.3	349	2	S67858	probable glutathio
290	6	4.3	304	2	G85714	hypothetical prote	363	6	4.3	351	1	C69198	gumI protein - Xan
291	6	4.3	305	1	S52775	hypothetical prote	364	6	4.3	352	2	S67935	phospho-N-acetylmu
292	6	4.3	308	2	B84311	hypothetical prote	365	6	4.3	353	2	B36963	branched-chain ket
293	6	4.3	311	2	AH2804	hypothetical prote	366	6	4.3	353	2	S29788	bcsA 5'--region pro
294	6	4.3	313	2	AD0920	conserved hypotet	367	6	4.3	353	2	S41958	glucose 1-dehydrog
295	6	4.3	313	2	H97583	porphobilinogen de	368	6	4.3	353	2	S29788	pupal cuticicle pro
296	6	4.3	316	2	H95960	hypothetical prote	369	6	4.3	355	2	T10722	anthocyanidin synt
297	6	4.3	316	2	G97465	lysar type transcri	370	6	4.3	355	2	A72279	sugar ABC transpor
298	6	4.3	317	2	B72395	hypothetical prote	371	6	4.3	357	1	QQMSLL	retrovirus-related
299	6	4.3	319	2	E97815	alcohol dehydrogen	372	6	4.3	358	2	S65163	hypothetical prote
300	6	4.3	321	2	B64797	protein FAN2.12 [i	373	6	4.3	359	2	T42087	probable 6-phospho
301	6	4.3	321	2	B87797	lipic acid synthet	374	6	4.3	361	2	T17282	hypothetical prote
302	6	4.3	321	2	F85562	lipote synthesis,	375	6	4.3	361	2	IS0475	hypothetical prote
303	6	4.3	321	2	T06845	hypothetical prote	376	6	4.3	364	1	S77360	dopamine D1 recept
304	6	4.3	322	2	H64933	succinylglutamate	377	6	4.3	364	1	C87125	chiD protein - Syn
305	6	4.3	322	2	B90935	hypothetical prote	378	6	4.3	365	2	T15010	hypothetical prote
306	6	4.3	322	2	F85783	hypothetical prote	379	6	4.3	365	2	E83710	hypothetical prote
307	6	4.3	322	2	T22403	hypothetical prote	380	6	4.3	367	2	T09376	hypothetical prote
308	6	4.3	323	2	G87358	dienelactone hydro	381	6	4.3	368	2	T05542	hypothetical prote
309	6	4.3	325	2	A82669	oxidative stress t	382	6	4.3	368	2	T40115	uv excision repair
310	6	4.3	325	2	S57977	CCCH zinc finger p	383	6	4.3	369	2	T06723	hypothetical prote
311	6	4.3	327	2	D90530	hypothetical prote	384	6	4.3	369	2	AC2702	outer membrane pro
312	6	4.3	328	2	C64570	phenylalanine-tRNA	385	6	4.3	369	2	C97484	outer membrane pro
313	6	4.3	328	2	E71863	phenylalanine-tRNA	386	6	4.3	369	2	H87633	threonine aldolase
314	6	4.3	328	2	T20856	hypothetical prote	387	6	4.3	370	2	B69029	pre-mRNA splicing
315	6	4.3	329	2	H83907	hypothetical prote	388	6	4.3	370	2	AD2375	hypothetical prote
316	6	4.3	329	2	C96033	cytochrome aa3 qui	389	6	4.3	370	2	H69291	conserved hypotet
317	6	4.3	329	2	probable regulator		390	6	4.3	371	2	T15095	hypothetical prote
318	6	4.3	329	2	AH3617	1-carboxy-3-chloro	391	6	4.3	371	2	T01303	hypothetical prote
319	6	4.3	330	2	T02525	probable DOF zinc	392	6	4.3	371	2	D84186	hypothetical prote
320	6	4.3	331	1	S44304	Phenol 2-mcnooxyge	393	6	4.3	371	2	H81303	branched-chain ami
321	6	4.3	331	1	B37831	Phenol 2-mcnooxyge	394	6	4.3	374	2	T36641	probable ABC-type

395	6	4.3	374	2	E90454	hypothetical prote	468	6	4.3	433	2	D90176	hypothetical prote
396	6	4.3	374	2	F96702	hypothetical prote	469	6	4.3	434	2	S28312	hypothetical prote
397	6	4.3	376	2	T35085	hypothetical prote	470	6	4.3	434	2	B69271	hypothetical prote
398	6	4.3	376	2	G90347	transposase ISC131	471	6	4.3	437	2	AH3285	gcpE protein [impo
399	6	4.3	377	2	F97267	uncharacterized co	472	6	4.3	437	2	H96933	aspartate kinase [
400	6	4.3	378	2	T06744	hypothetical prote	473	6	4.3	438	2	S73952	adhesin P1 precurs
401	6	4.3	380	1	W22MP	dihydrodipicolinat	474	6	4.3	438	2	S71157	cytochrome c bioge
402	6	4.3	380	2	T05220	hypothetical prote	475	6	4.3	440	2	G72317	chromosome c bioge
403	6	4.3	381	2	G71130	hypothetical prote	476	6	4.3	440	2	AH1395	conserved hypothet
404	6	4.3	383	2	S53716	delta-like homeoti	477	6	4.3	440	2	AH1770	conserved hypothet
405	6	4.3	384	2	D87471	ROK family protein	478	6	4.3	441	2	H92617	folylpolyglutamate
406	6	4.3	385	2	T21756	hypothetical prote	479	6	4.3	444	2	E96584	hypothetical prote
407	6	4.3	385	2	JC7751	exo-alpha-sialidas	480	6	4.3	446	1	DXH0D1	dopamine receptor
408	6	4.3	386	2	T12048	ribosomal protein	481	6	4.3	446	2	I47217	dopamine receptor
409	6	4.3	386	2	S72168	dopamine receptor	482	6	4.3	446	2	G87448	succinylarginine d
410	6	4.3	387	2	E71711	probable o-sialogl	483	6	4.3	447	2	T13091	probable minor cap
411	6	4.3	387	2	C82336	conserved hypothet	484	6	4.3	449	2	A30303	interferon-related
412	6	4.3	387	2	H64182	xylose operon regl	485	6	4.3	449	2	A44989	interferon-related
413	6	4.3	388	2	E84025	hypothetical prote	486	6	4.3	449	2	JC7306	extracellular prot
414	6	4.3	389	2	T30216	hypothetical prote	487	6	4.3	450	2	A55886	dopamine receptor
415	6	4.3	390	2	T25642	hypothetical prote	488	6	4.3	451	2	I51659	dopamine D1A recep
416	6	4.3	391	2	H90308	transposase ISC131	489	6	4.3	451	2	F75131	hypothetical prote
417	6	4.3	393	2	D70539	probable citrate s	490	6	4.3	451	2	C75075	hypothetical prote
418	6	4.3	393	2	E90272	transposase ISC131	491	6	4.3	454	2	C82941	ATP synthase beta
419	6	4.3	393	2	AE1754	portal protein [ba	492	6	4.3	454	2	H90980	probable amino aci
420	6	4.3	394	2	T08757	probable translati	493	6	4.3	454	2	E5826	probable amino aci
421	6	4.3	394	2	S74643	proteinase hbaA (E	494	6	4.3	454	2	E64966	probable amino aci
422	6	4.3	394	2	G83027	conserved hypothet	495	6	4.3	454	2	AG0783	probable amino aci
423	6	4.3	395	2	T38685	probable cysteine	496	6	4.3	454	2	C85173	thiophene and fura
424	6	4.3	395	2	C90328	transposase ISC131	497	6	4.3	454	2	A98209	hypothetical prote
425	6	4.3	396	2	S55281	translation elonga	498	6	4.3	454	2	C86055	hypothetical prote
426	6	4.3	396	2	S27870	house-keeping prot	499	6	4.3	454	2	AE0957	thiophene and fura
427	6	4.3	397	2	A82854	flavohemoprotein X	500	6	4.3	454	2	T02680	hypothetical prote
428	6	4.3	397	2	A75137	hypothetical prote	501	6	4.3	457	2	I51660	dopamine D1B recep
429	6	4.3	399	1	S76745	hypothetical prote	502	6	4.3	458	2	A44487	probable replicati
430	6	4.3	399	2	F69034	argininosuccinate	503	6	4.3	458	2	S24457	hypothetical prote
431	6	4.3	399	2	C90455	transposase ISC131	504	6	4.3	459	2	D34791	interleukin-7 rece
432	6	4.3	400	2	S32804	beta-3-adrenergic	505	6	4.3	459	2	A56849	dopamine receptor-
433	6	4.3	401	2	F97260	uncharacterized co	506	6	4.3	459	2	D70717	hypothetical prote
434	6	4.3	402	1	E64822	probable membrane	507	6	4.3	459	2	T31608	hypothetical prote
435	6	4.3	402	2	A85595	probable DEOR-type	508	6	4.3	459	2	T31608	hypothetical prote
436	6	4.3	402	2	E90744	probable DEOR-type	509	6	4.3	460	2	H96536	hypothetical prote
437	6	4.3	402	2	A70882	probable PPE prote	510	6	4.3	461	2	T36599	probable beta-lact
438	6	4.3	403	2	E90290	transposase ISC131	511	6	4.3	462	2	C83920	dopamine receptor-
439	6	4.3	404	2	AB1336	argininosuccinate	512	6	4.3	462	2	C83920	hypothetical prote
440	6	4.3	404	2	AH1706	argininosuccinate	513	6	4.3	465	2	I51661	dopamine D1C recep
441	6	4.3	404	2	S45923	probable phosphopa	514	6	4.3	469	2	T50934	dioxynase D1A1,
442	6	4.3	404	2	S42831	F40R12.2 protein -	515	6	4.3	469	2	D72722	probable MRSA prot
443	6	4.3	406	2	T48103	mRNA binding prote	516	6	4.3	470	2	A52155	hypothetical prote
444	6	4.3	407	2	T48308	60S ribosomal prot	517	6	4.3	471	2	S35635	DNA injection prot
445	6	4.3	408	2	C66903	hypothetical prote	518	6	4.3	472	2	AG3600	cellulose synthase
446	6	4.3	408	2	E90326	transposase ISC131	519	6	4.3	473	2	D81782	oxygen-independent
447	6	4.3	410	1	S68153	cellulase [EC 3.2.	520	6	4.3	473	2	H81204	oxygen-independent
448	6	4.3	411	2	C90458	transposase ISC131	521	6	4.3	474	2	T31770	hypothetical prote
449	6	4.3	411	2	AG3003	conserved hypothet	522	6	4.3	474	2	T10271	capsid-associated
450	6	4.3	411	2	B98280	hypothetical prote	523	6	4.3	475	2	T27811	hypothetical prote
451	6	4.3	413	1	S34305	modulation protein	524	6	4.3	476	2	A70704	probable rocf prot
452	6	4.3	413	2	I28602	translation releas	525	6	4.3	480	2	G84360	phenylalanine-tRNA
453	6	4.3	414	2	D68547	protein F02A9.4b [526	6	4.3	481	2	T03660	phosphoglycerate x
454	6	4.3	416	2	F71379	heat shock protein	527	6	4.3	481	2	S74934	pleD-1 protein - S
455	6	4.3	416	2	S76310	hypothetical prote	528	6	4.3	485	2	B88114	protein F53C3.9 [i
456	6	4.3	417	2	S57820	pyruvate decarboxy	529	6	4.3	485	2	C75460	hypothetical prote
457	6	4.3	417	2	T24618	hypothetical prote	530	6	4.3	486	2	I39523	dehydroshikimate d
458	6	4.3	421	2	T41577	pombe specific con	531	6	4.3	486	2	T38174	probable CCS1/GLO3
459	6	4.3	423	2	T50923	acetylnitrothine tr	532	6	4.3	487	1	DXRTD1	dopamine receptor
460	6	4.3	423	2	AI3309	tRNA adenylyltrans	533	6	4.3	488	2	T41160	hypothetical prote
461	6	4.3	424	2	G83733	hypothetical prote	534	6	4.3	490	2	F38462	S-mephenytoin 4'-h
462	6	4.3	425	2	T16433	hypothetical prote	535	6	4.3	490	2	T06714	probable cytochrom
463	6	4.3	426	2	I48379	gene hb protein -	536	6	4.3	490	2	G85354	hypothetical prote
464	6	4.3	426	2	A12498	L-amino acid oxida	537	6	4.3	490	2	E71486	probable s/t prote
465	6	4.3	428	2	S73379	adhesin p1 precurs	538	6	4.3	490	2	F70538	probable ppdk prot
466	6	4.3	432	2	B84127	hypothetical prote	539	6	4.3	491	1	F08H08	fibrinogen beta ch
467	6	4.3	433	1	E64242	GTP-binding protei	540	6	4.3	491	2	C83206	probable outer mem

541	6	4.3	492	2	D70649	cytochrome P450 Rv	614	6	4.3	578	2	H75256	malate oxidoreduct
542	6	4.3	492	2	G70899	probable monooxyge	615	6	4.3	581	2	A49073	HSN motor neurons
543	6	4.3	492	2	T32685	hypothetical prote	616	6	4.3	581	2	C86430	hypothetical prote
544	6	4.3	495	2	S43294	bone morphogenetic	617	6	4.3	589	2	JG0196	protein kinase DYR
545	6	4.3	495	2	S75340	NADH2 dehydrogenas	618	6	4.3	590	2	S16411	terminase ATPase c
546	6	4.3	496	2	E90181	hypothetical prote	619	6	4.3	591	2	P95084	pyruvate oxidase l
547	6	4.3	497	2	T27012	hypothetical prote	620	6	4.3	591	2	B97952	pyruvate oxidase l
548	6	4.3	498	2	T40776	MSF membrane trans	621	6	4.3	592	2	D70863	hypothetical prote
549	6	4.3	499	1	C44767	benzoylformate dec	622	6	4.3	592	2	T34446	pyruvate, phosphat
550	6	4.3	499	2	T47722	probable protein k	623	6	4.3	601	2	E87028	protein W03F9.10 l
551	6	4.3	500	1	E9FF	zip protein precur	624	6	4.3	602	2	A88923	hypothetical prote
552	6	4.3	500	2	J67668	dipeptidyl-peptida	625	6	4.3	602	2	E90902	glucan 1,4-alpha-g
553	6	4.3	500	2	J67668	hypothetical prote	626	6	4.3	604	1	JP0001	hypothetical prote
554	6	4.3	501	2	A55452	cartilage-derived	627	6	4.3	605	1	S48940	hypothetical prote
555	6	4.3	501	2	JC2347	growth/differentia	628	6	4.3	607	1	S42639	Arr-dependent RNA
556	6	4.3	504	2	T04810	aspartate-TRNA lig	629	6	4.3	609	2	A96693	probable receptor
557	6	4.3	504	2	B70821	hypothetical prote	630	6	4.3	611	2	T15059	hypothetical prote
558	6	4.3	506	2	AB3411	cysteine-TRNA liga	631	6	4.3	614	2	S43427	intermediate filam
559	6	4.3	507	2	AG3187	aldohyde dehydroge	632	6	4.3	614	2	B69332	conserved hypotet
560	6	4.3	508	2	B30310	glucose transport	633	6	4.3	615	2	A83188	hypothetical prote
561	6	4.3	509	1	TVHAST	protein-tyrosine k	634	6	4.3	616	2	H90764	hypothetical prote
562	6	4.3	509	2	A32101	glucose transport	635	6	4.3	616	2	P90911	hypothetical prote
563	6	4.3	509	2	A33801	muscle-fat glucose	636	6	4.3	616	2	F85627	hypothetical prote
564	6	4.3	509	2	S74935	hypothetical prote	637	6	4.3	617	2	F71359	proline-TRNA ligas
565	6	4.3	510	2	H81369	purH bifunctional	638	6	4.3	617	2	B90851	hypothetical prote
566	6	4.3	511	2	G95394	probable oxygenase	639	6	4.3	617	2	A90874	hypothetical prote
567	6	4.3	511	2	T48777	6-HYDROXY-D-NICOTI	640	6	4.3	617	2	B91066	hypothetical prote
568	6	4.3	511	2	T23354	hypothetical prote	641	6	4.3	617	2	B85679	unknown protein en
569	6	4.3	512	2	S61905	threonine synthase	642	6	4.3	617	2	H85819	unknown protein en
570	6	4.3	514	1	QJWNPB	photosystem II chl	643	6	4.3	618	2	F84409	arsenite transport
571	6	4.3	515	2	H84013	hypothetical prote	644	6	4.3	620	2	AH1827	alpha-amyase (imp
572	6	4.3	516	2	T40631	probable membrane	645	6	4.3	620	2	B96933	amino acid transpo
573	6	4.3	516	2	F96549	hypothetical prote	646	6	4.3	621	2	T20307	hypothetical prote
574	6	4.3	516	2	F83894	hypothetical prote	647	6	4.3	624	2	D64449	threonine-TRNA lig
575	6	4.3	516	2	G95406	probable ABC trans	648	6	4.3	629	2	A69814	ABC transporter (A
576	6	4.3	517	2	H87022	hypothetical prote	649	6	4.3	629	2	JG0195	protein kinase DYR
577	6	4.3	519	2	T45447	probable two-compo	650	6	4.3	630	2	C39930	hypothetical prote
578	6	4.3	519	2	T23739	hypothetical prote	651	6	4.3	630	2	T38637	hypothetical prote
579	6	4.3	523	2	S42727	translation initia	652	6	4.3	630	2	A39344	tumor-associated m
580	6	4.3	524	2	S71961	translation initia	653	6	4.3	630	2	AC1129	Internalin B (impo
581	6	4.3	524	2	F87664	glycine cleavage s	654	6	4.3	631	2	I52257	episialin - mouse
582	6	4.3	524	2	JC7090	germ cell-less pro	655	6	4.3	632	2	G69306	NADH oxidase (noxB
583	6	4.3	525	2	A36130	transcription init	656	6	4.3	632	2	E69407	NADH oxidase (noxB
584	6	4.3	526	2	T33779	hypothetical prote	657	6	4.3	632	2	B69310	mRNA 3'-end proces
585	6	4.3	528	2	T00951	probable 3-oxoacyl	658	6	4.3	633	2	H96748	unknown protein Tl
586	6	4.3	532	2	S66087	amino acid transpo	659	6	4.3	633	2	T24898	hypothetical prote
587	6	4.3	532	2	T18571	probable cycloprop	660	6	4.3	634	2	T18711	hypothetical prote
588	6	4.3	532	2	H72730	probable acyl-CoA	661	6	4.3	634	2	T18702	hypothetical prote
589	6	4.3	534	2	C70548	probable regulator	662	6	4.3	635	2	T34866	hypothetical prote
590	6	4.3	537	2	AB2766	sulfate permease l	663	6	4.3	638	2	T43018	snail protein - fi
591	6	4.3	537	2	F97546	hypothetical prote	664	6	4.3	642	2	F72528	probable Glu-tRNA
592	6	4.3	539	2	T50579	probable membrane	665	6	4.3	645	2	H89951	threonyl-TRNA synt
593	6	4.3	540	2	A95264	probable ABC trans	666	6	4.3	645	2	G01205	serine/threonine p
594	6	4.3	542	2	T20457	hypothetical prote	667	6	4.3	652	2	T39722	methyl-accepting c
595	6	4.3	543	2	E88280	protein egl-43 (im	668	6	4.3	654	2	A69656	hypothetical prote
596	6	4.3	544	2	A55146	guanine nucleotide	669	6	4.3	656	2	B70766	extracellular solu
597	6	4.3	545	2	T52068	RAN GTPase-activa	670	6	4.3	659	2	D75450	hypothetical prote
598	6	4.3	547	2	AC2541	dihydroxy-acid deh	671	6	4.3	659	2	S77658	hypothetical prote
599	6	4.3	554	2	E72362	hypothetical prote	672	6	4.3	660	2	T40781	26S proteinase sub
600	6	4.3	556	2	T28960	hypothetical prote	673	6	4.3	661	2	F70751	hypothetical prote
601	6	4.3	556	2	T40077	hypothetical prote	674	6	4.3	666	2	H75295	transketolase - De
602	6	4.3	557	2	AC2137	ABC transporter AT	675	6	4.3	672	2	T20310	hypothetical prote
603	6	4.3	562	2	A94297	probable lipote-p	676	6	4.3	674	2	T23235	hypothetical prote
604	6	4.3	562	2	C86138	probable lipote-p	677	6	4.3	677	2	T19281	hypothetical prote
605	6	4.3	563	2	B82579	peptide synthase X	678	6	4.3	680	2	A42298	thimet oligopeptid
606	6	4.3	567	2	S63778	adhesin AP65-1 pre	679	6	4.3	680	2	S47718	oligopeptidase A (
607	6	4.3	567	2	AC0143	choline dehydrogen	680	6	4.3	680	2	B86021	oligopeptidase A (
608	6	4.3	567	2	T28797	hypothetical prote	681	6	4.3	680	2	B91175	oligopeptidase A (
609	6	4.3	569	2	D96954	methyl-accepting c	682	6	4.3	680	2	AB0988	oligopeptidase A (
610	6	4.3	570	2	G73595	hypothetical prote	683	6	4.3	680	2	T41670	hypothetical prote
611	6	4.3	571	2	C75530	conserved hypotet	684	6	4.3	683	2	A39784	phycobilisome anch
612	6	4.3	576	2	T22700	hypothetical prote	685	6	4.3	685	2	AH3414	soluble lytic mure
613	6	4.3	577	2	T40297	membrane transport	686	6	4.3	691	2	T32748	hypothetical prote

587	6	4.3	692	2	C87644	fatty oxidation co	760	6	4.3	857	2	T14471	probable S-recepto
588	6	4.3	692	2	D86547	hypothetical prote	761	6	4.3	858	1	VCLJG2	env polypeptide pr
589	6	4.3	692	2	A81593	hypothetical prote	762	6	4.3	859	2	T00434	probable kinesin h
590	6	4.3	693	2	T39154	probable ABC trans	763	6	4.3	869	2	H89775	alcohol-acetaldehy
591	6	4.3	694	2	A95866	probable transketo	764	6	4.3	876	2	B96693	probable receptor
592	6	4.3	695	2	B84495	hypothetical prote	765	6	4.3	878	2	AE0478	phosphoenolpyruvat
593	6	4.3	697	2	D84429	hypothetical prote	766	6	4.3	880	2	A55201	meiosis-specific p
594	6	4.3	701	2	D83677	hypothetical prote	767	6	4.3	881	1	WZBSE9	DNA helicase/prima
595	6	4.3	705	2	D84680	probable ABC trans	768	6	4.3	893	2	T42600	99.5K DNA helicase
596	6	4.3	705	2	T34531	hypothetical prote	769	6	4.3	893	2	H95953	probable bifunctio
597	6	4.3	708	2	T19474	hypothetical prote	770	6	4.3	897	2	T06540	polyribonucleotide
598	6	4.3	708	2	T29669	hypothetical prote	771	6	4.3	900	2	A95340	cation transport p
599	6	4.3	710	2	T00055	hypothetical prote	772	6	4.3	902	2	T49878	respiratory burst
600	6	4.3	712	2	A12514	ABC transporter At	773	6	4.3	905	2	T00475	probable disease r
701	6	4.3	723	2	S51788	malate synthase (E	774	6	4.3	905	2	T23510	hypothetical prote
702	6	4.3	724	2	H87423	cation-transportin	775	6	4.3	905	2	T23229	hypothetical prote
703	6	4.3	724	2	C28332	DNA ligase Adu2082	776	6	4.3	907	2	A45560	sporozoite surface
704	6	4.3	724	2	G97609	DNA ligase (polyde	777	6	4.3	910	2	D75524	alpha-dextran endo
705	6	4.3	727	2	T29612	hypothetical prote	778	6	4.3	914	2	T25220	hypothetical prote
706	6	4.3	730	2	T05345	hypothetical prote	779	6	4.3	916	2	G82993	probable ATP-bind
707	6	4.3	731	2	T04629	hypothetical prote	780	6	4.3	921	2	F84593	hypothetical prote
708	6	4.3	733	2	AD2444	hypothetical prote	781	6	4.3	926	2	T39082	hypothetical prote
709	6	4.3	736	2	B82944	ribose/galactose A	782	6	4.3	932	2	T48761	hypothetical prote
710	6	4.3	741	2	A28572	bsg25D protein f	783	6	4.3	936	2	T06190	lipoxigenase (SC 1
711	6	4.3	743	2	C86168	hypothetical prote	784	6	4.3	938	2	H83050	probable ferredoxi
712	6	4.3	743	2	A29232	101K malaria antig	785	6	4.3	942	2	T39624	6-phosphofructokin
713	6	4.3	744	2	AF0410	GTP diphosphokinas	786	6	4.3	947	2	T08605	hypothetical prote
714	6	4.3	744	2	A92582	malate synthase G	787	6	4.3	955	2	T48515	hypothetical prote
715	6	4.3	744	2	F97364	malate synthase G	788	6	4.3	961	2	A55380	faciogenital dyspl
716	6	4.3	747	2	D95862	probable sensor hi	789	6	4.3	963	2	T48707	related to regulat
717	6	4.3	748	2	AD0866	phosphoenolpyruvat	790	6	4.3	980	2	A38523	genome polypeptid
718	6	4.3	749	2	S75331	penicillin-binding	791	6	4.3	981	2	T16060	hypothetical prote
719	6	4.3	750	2	T42614	probable envelope	792	6	4.3	990	2	T11612	hypothetical prote
720	6	4.3	750	2	A84315	malate dehydrogena	793	6	4.3	994	2	T21356	hypothetical prote
721	6	4.3	751	2	F83080	hypothetical prote	794	6	4.3	996	2	T21356	hypothetical prote
722	6	4.3	755	2	H86561	Ct456 hypothetical	795	6	4.3	997	2	JE0237	apolipoprotein E r
723	6	4.3	755	2	T72061	hypothetical prote	796	6	4.3	997	2	T15243	hypothetical prote
724	6	4.3	759	2	I38593	fibroblast activat	797	6	4.3	1001	2	T29105	myosin-B - Toxopla
725	6	4.3	762	2	H87302	chemotaxis protein	798	6	4.3	1002	2	T30546	major surface glyc
726	6	4.3	763	2	T21006	hypothetical prote	799	6	4.3	1007	2	T24543	hypothetical prote
727	6	4.3	764	2	F83431	periplasmic beta-g	800	6	4.3	1011	2	T20785	hypothetical prote
728	6	4.3	769	2	A71403	probable transport	801	6	4.3	1013	2	T33470	hypothetical prote
729	6	4.3	769	2	F87486	outer membrane pro	802	6	4.3	1014	2	T30545	major surface glyc
730	6	4.3	773	2	T44989	transducer protein	803	6	4.3	1016	2	T31343	proline dehydrogen
731	6	4.3	776	2	A45583	neuroendocrine-spe	804	6	4.3	1017	2	T30195	DNA-directed DNA p
732	6	4.3	778	2	H84678	hypothetical prote	805	6	4.3	1018	2	T40353	hypothetical prote
733	6	4.3	783	2	B83232	conserved hypotet	806	6	4.3	1021	2	T23352	hypothetical prote
734	6	4.3	783	2	T35389	probable serine-th	807	6	4.3	1027	2	F87370	alpha-L-rhamnosida
735	6	4.3	788	1	Q8BEE3	DNA repair protein	808	6	4.3	1029	2	T05050	protein kinase hom
736	6	4.3	788	1	Q8BEE3	HHuF1 protein - hu	809	6	4.3	1048	2	T23764	hypothetical prote
737	6	4.3	788	1	I51530	integrin beta-3 su	810	6	4.3	1051	2	T05426	hypothetical prote
738	6	4.3	789	1	A45617	6-phosphofructokin	811	6	4.3	1053	2	B70987	probable PPE prote
739	6	4.3	790	2	T34293	hypothetical prote	812	6	4.3	1060	2	B83547	kinesin-related pr
740	6	4.3	791	2	C95335	hypothetical prote	813	6	4.3	1062	2	H83566	proline dehydrogen
741	6	4.3	792	1	EAHU	elastin precursor,	814	6	4.3	1062	2	T38122	carbamoyl-phosphat
742	6	4.3	793	2	AB1750	exoribonuclease RN	815	6	4.3	1076	2	H83966	hypothetical prote
743	6	4.3	793	2	AB1380	exoribonuclease RN	816	6	4.3	1081	2	T09837	sucrose-phosphate
744	6	4.3	795	2	T49835	hypothetical prote	817	6	4.3	1091	1	IJCJNL	neural cell adhesi
745	6	4.3	795	2	T20609	hypothetical prote	818	6	4.3	1095	2	T20528	hypothetical prote
746	6	4.3	796	2	T21460	hypothetical prote	819	6	4.3	1098	2	T29106	myosin-C - Toxopla
747	6	4.3	799	2	S65192	hypothetical prote	820	6	4.3	1119	2	B86340	protein P210.24 (
748	6	4.3	802	2	T21315	hypothetical prote	821	6	4.3	1120	2	B83498	conserved hypotet
749	6	4.3	809	2	F87458	conserved hypotet	822	6	4.3	1134	1	A29944	chaoptin precursor
750	6	4.3	811	2	T19974	hypothetical prote	823	6	4.3	1145	1	GNLJEW	HIV-1 retropepsin
751	6	4.3	813	2	AF0526	ATP-dependent heli	824	6	4.3	1146	1	GNLJEW	HIV-1 retropepsin
752	6	4.3	815	2	JG0197	myosin-light-chain	825	6	4.3	1155	2	G87477	transcription-repa
753	6	4.3	829	2	A34692	ecdysone-induced p	826	6	4.3	1161	2	S57180	probable membrane
754	6	4.3	835	2	A40971	DNA-binding protei	827	6	4.3	1172	2	T00065	hypothetical prote
755	6	4.3	836	2	A15237	conserved hypotet	828	6	4.3	1176	2	A33856	surface-layer 125K
756	6	4.3	837	2	T71027	hypothetical prote	829	6	4.3	1176	2	A49848	nitrite reductase
757	6	4.3	845	2	T34064	hypothetical prote	830	6	4.3	1186	2	S35993	DNA repair protein
758	6	4.3	846	1	Q8BEC3	HORRI protein - hu	831	6	4.3	1196	2	S35994	DNA repair protein
759	6	4.3	850	2	T14472	S-receptor kinase	832	6	4.3	1202	2	T17197	adenylate cyclase

833	6	4.3	1206	2	F72233	conserved hypothet	906	6	4.3	3766	2	T29165	hypothetical prote
834	6	4.3	1207	2	B88789	protein ZK1251.9 (907	6	4.3	3972	2	S75251	hypothetical prote
835	6	4.3	1208	2	T23754	hypothetical prote	908	6	4.3	4151	2	T13734	apolipoprotein B-1
836	6	4.3	1211	2	T23210	hypothetical prote	909	6	4.3	4563	1	LPUB	hypothetical coile
837	6	4.3	1212	2	T00270	co-repressor prote	910	6	4.3	4717	2	T41581	probable membrane
838	6	4.3	1219	2	T161713	hypothetical prote	911	6	4.3	4910	2	S64942	ALR protein - huma
839	6	4.3	1220	1	DJBEC3	DNA-directed DNA p	912	6	4.3	4957	2	T03455	ALR protein - huma
840	6	4.3	1223	2	T42573	protein B0361.3 [i	913	6	4.3	5262	2	T03454	polyketide synthas
841	6	4.3	1224	2	C86504	hypothetical prote	914	6	4.3	5563	2	T03226	T-cell receptor be
842	6	4.3	1224	2	S40977	DNA-directed RNA p	915	5	3.5	10	2	PH0895	bradykinin-potenti
843	6	4.3	1224	2	S73171	hypothetical prote	916	5	3.5	11	2	C37196	bradykinin-potenti
844	6	4.3	1227	2	T48028	DNA-directed RNA p	917	5	3.5	15	2	D37196	lipid transfer pro
845	6	4.3	1228	2	I40468	hypothetical prote	918	5	3.5	15	2	A53085	T-cell receptor al
846	6	4.3	1229	2	T25697	surface layer prot	919	5	3.5	16	2	F41299	hypothetical prote
847	6	4.3	1229	2	A56068	hypothetical prote	920	5	3.5	20	2	T01691	uroporphyrinogen d
848	6	4.3	1234	2	T31823	co-repressor prote	921	5	3.5	27	2	S35595	alpha-1 type-1 col
849	6	4.3	1235	2	T13710	hypothetical prote	922	5	3.5	28	2	I50169	hypothetical prote
850	6	4.3	1239	2	I49705	protein-tyrosine k	923	5	3.5	30	2	C82341	ilvGMDA operon le
851	6	4.3	1251	2	T21389	glutamate receptor	924	5	3.5	32	1	LFEBIT	ilvGMDA operon le
852	6	4.3	1252	2	T00263	hypothetical prote	925	5	3.5	32	1	LFEBIT	ilvGMDA operon le
853	6	4.3	1255	2	T06267	hypothetical prote	926	5	3.5	32	2	E27480	cyclochrome-c3 hydr
854	6	4.3	1265	2	T12782	nematodes resistan	927	5	3.5	32	2	E91216	ilvGMDA operon le
855	6	4.3	1270	2	T13813	hypothetical prote	928	5	3.5	32	2	F86062	ilvGMDA operon le
856	6	4.3	1290	2	T00018	period protein hom	929	5	3.5	32	2	AG0924	ilvGMDA operon at
857	6	4.3	1296	1	HMS01F	aggregation protei	930	5	3.5	34	2	D81044	hypothetical prote
858	6	4.3	1305	2	A40879	phospholipase C (B	931	5	3.5	36	2	C82475	hypothetical prote
859	6	4.3	1305	2	H41562	150K mating aggreg	932	5	3.5	39	2	S65949	hypothetical prote
860	6	4.3	1306	2	S22624	aggregation protei	933	5	3.5	39	2	B55980	hypothetical prote
861	6	4.3	1312	1	B40879	phospholipase C (B	934	5	3.5	41	2	C50208	hypothetical prote
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863	6	4.3	1316	2	S31146	[beta]' subunit of	936	5	3.5	42	2	PD032	hypothetical prote
864	6	4.3	1335	2	T18289	DNA-directed RNA p	937	5	3.5	43	1	ZD5P79	RhPI-alpha polypep
865	6	4.3	1335	2	S27812	racGAP protein - s	938	5	3.5	45	2	E70236	Gene 55.4 protein
866	6	4.3	1348	2	A43917	probable epidermal	939	5	3.5	45	2	T02336	hypothetical prote
867	6	4.3	1356	2	F84486	probable epidermal	940	5	3.5	45	2	T52271	R4R3-MYB transcrip
868	6	4.3	1364	2	T00250	probable retroelem	941	5	3.5	45	2	T52272	R2R3-MYB transcrip
869	6	4.3	1392	2	T51547	MEG2 protein - hu	942	5	3.5	45	2	T52277	R2R3-MYB transcrip
870	6	4.3	1403	2	S64142	probable transcrip	943	5	3.5	48	2	S27128	histone H1 - sea u
871	6	4.3	1469	2	B36665	hypothetical prote	944	5	3.5	50	2	T06923	high light-inducib
872	6	4.3	1480	2	A36665	slit protein 2 pre	945	5	3.5	51	2	AG1060	aspartic proteinas
873	6	4.3	1489	2	A82524	slit protein 1 pre	946	5	3.5	52	2	T00141	hypothetical prote
874	6	4.3	1493	2	A38218	glutamate synthase	947	5	3.5	52	2	F97078	hypothetical prote
875	6	4.3	1526	2	T41522	GAP-associated pro	948	5	3.5	52	2	AC1894	hypothetical prote
876	6	4.3	1551	2	T18941	myosin ii - fissio	949	5	3.5	54	1	BGSB	hypothetical prote
877	6	4.3	1589	1	RGBYC5	hypothetical prote	950	5	3.5	54	2	A82579	spermatid transiti
878	6	4.3	1589	2	T13606	cell division cont	951	5	3.5	55	1	BQBO	spermatid transiti
879	6	4.3	1589	2	C44766	hypothetical prote	952	5	3.5	56	2	AC2100	CAB/ELIP/HLIP-rela
880	6	4.3	1639	2	T14181	defective chorion-	953	5	3.5	56	2	A95955	hypothetical prote
881	6	4.3	1655	2	T13998	peptide synthetase	954	5	3.5	57	2	H84366	hypothetical prote
882	6	4.3	1706	2	B75633	gene mastermind pr	955	5	3.5	57	2	A49300	hypothetical prote
883	6	4.3	1711	1	A55148	probable RNA helic	956	5	3.5	57	2	AG0134	hypothetical prote
884	6	4.3	1731	2	AB3045	protein-tyrosine-p	957	5	3.5	58	1	TVHUB	hypothetical prote
885	6	4.3	1731	2	B98241	ice nucleation pro	958	5	3.5	58	2	C84363	transforming prote
886	6	4.3	1839	1	OFBTK	hypothetical prote	959	5	3.5	58	2	AE1868	ferredoxin (import
887	6	4.3	1921	2	T13827	adenylate cyclase	960	5	3.5	59	2	G71717	hypothetical prote
888	6	4.3	2108	2	H70819	kinesin-73 - fruit	961	5	3.5	60	2	C29606	hypothetical prote
889	6	4.3	2123	2	S55089	probable polyketid	962	5	3.5	61	2	AT0460	hypothetical prote
890	6	4.3	2204	1	RRNZV	probable acetyl-Co	963	5	3.5	62	2	JT06878	hypothetical prote
891	6	4.3	2244	2	T08212	genome polyprotein	964	5	3.5	62	2	AP3474	tyrocidine synthet
892	6	4.3	2348	2	AD1841	RNA-directed RNA p	965	5	3.5	62	2	F84284	ubiquinol-cytochro
893	6	4.3	2396	2	T13714	hypothetical prote	966	5	3.5	63	2	F84284	ubiquinol-cytochro
894	6	4.3	2500	2	G88493	kakapo gene protei	967	5	3.5	63	2	T43546	DNA-directed RNA p
895	6	4.3	2524	2	A35844	protein F57B9.2 [i	968	5	3.5	63	2	T52536	DNA-directed RNA p
896	6	4.3	2555	2	A40043	Xotch protein - Af	969	5	3.5	65	2	G69542	hypothetical prote
897	6	4.3	2569	2	T14164	notch protein homo	970	5	3.5	65	2	T42904	hypothetical prote
898	6	4.3	2639	2	T31128	peptide synthetase	971	5	3.5	65	2	S77379	hypothetical prote
899	6	4.3	2670	2	A46719	fibroin - Chinese	972	5	3.5	65	2	H83679	hypothetical prote
900	6	4.3	2671	2	A49873	inositol 1,4,5-tri	973	5	3.5	66	2	H87276	hypothetical prote
901	6	4.3	2833	2	A43360	inositol 1,4,5-tri	974	5	3.5	66	2	AH0076	hypothetical prote
902	6	4.3	2918	2	A54105	inositol 1,4,5-tri	975	5	3.5	66	2	T08651	hypothetical prote
903	6	4.3	3172	2	S22012	fibroin-2 precu	976	5	3.5	67	2	B56888	hypothetical prote
904	6	4.3	3178	2	S13595	erythronolide synt	977	5	3.5	67	2	T17830	alkaline phosphata
905	6	4.3	3355	2	G81702	6-deoxyerythronol	978	5	3.5	67	2	H69981	hypothetical prote

A;Reference number: Z17931

RESULT 1

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C;Experimental source: Cultivar Columbia; BAC clone T28D5
C;Genetics:
A;Gene: ATSP:T28D5.100
A;Map position: 4

Query Match          5.7%; Score 8; DB 2; Length 707;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 SAIAATVT 66
    |||||
Db 41 SAIAATVT 48

RESULT 4
C72893
Hypothetical protein B2168_C2_205 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72893
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B2168.
A;Reference number: S72586
A;Accession: S72893
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <SMI>
A;Cross-references: EMBL:U00018; NID:G467037; PIDN:AAAI7229.1; PID:G467045
C;Genetics:
A;Start codon: GTG

Query Match          5.0%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ALAGMCG 49
    |||||
Db 42 ALAGMCG 48

RESULT 5
S73004
Hypothetical protein B229_F2_64 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S73004

```

R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B229.
A;Reference number: S72588
A;Accession: S73004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <SMI>
A;Cross-references: EMBL:U00020; NID:G467102; PIDN:AAAL7318.1; PID:G467136

Query Match 5.0%; Score 7; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 3 STSTTTN 9
|||||
DB 85 STSTTTN 91

RESULT 6

A40669
Mitochondrial receptor complex chain MOM22 - Neurospora crassa
N;Alternate names: mitochondrial outer membrane preprotein receptor chain MOM22
C;Species: Neurospora crassa
C;Date: 03-May-1994 #sequence_revision 02-Jun-1994 #text_change 22-Jun-1999
C;Accession: A40669; S33472
R;Kiebler, M.; Keil, P.; Schneider, H.; van der Klei, I.J.; Pfanner, N.; Neupert, W.
Cell 74, 483-492, 1993
A;Title: The mitochondrial receptor complex: a central role of MOM22 in mediating prepro
A;Reference number: A40669; MUID:93351229; PMID:8348615
A;Accession: A40669
A;Molecule type: mRNA
A;Residues: 1-154 <KIE>
A;Cross-references: GB:X71021; NID:G311426; PIDN:CAA50339.1; PID:G311427
C;Comment: This protein resides in the mitochondrial outer membrane (MOM) where it serve
C;Genetics:
C;Superfamily: mitochondrial receptor complex chain MOM22
C;Keywords: mitochondrion; transmembrane protein
F;85-105/Domain: transmembrane #status predicted <TMM>

Query Match 5.0%; Score 7; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 5 STTTNFV 11
|||||
DB 69 STTTNFV 75

RESULT 7

B57055
melanocortin-4 receptor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999
C;Accession: B57055
R;Yountjoy, K.G.; Mortrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.
Mol. Endocrinol. 8, 1298-1308, 1994
A;Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and autot
A;Reference number: A57055; MUID:95157557; PMID:7854347
A;Accession: B57055
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-215 <MOU>
C;Superfamily: melanocortin receptor

Query Match 5.0%; Score 7; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 24; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 52 VLPGTCA 58
|||||
DB 151 VLPGTGA 157

RESULT 8

A33619
Transcription regulator, gntR family BMEII0878 [imported] - Brucella melitensis (strai
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3619
R;DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliter
A;Reference number: AB3252; PMID:11756688
A;Accession: AB3619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAU54120.1; PID:G17985081; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0878
A;Map position: 11

Query Match 5.0%; Score 7; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 27; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 25 MREALLR 31
|||||
DB 69 MREALLR 75

RESULT 9

H71291
probable flagellar motor rotation protein (motB) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jun-2000
C;Accession: H71291
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71291
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <COL>
A;Cross-references: GB:AE001244; GB:AE000520; NID:G3323005; PIDN:AAAC5689.1; PID:G33230
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: Tp0724
C;Superfamily: probably motility protein ytxE

Query Match 5.0%; Score 7; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 27; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 26 REALLRV 32
|||||
DB 138 REALLRV 144

RESULT 10

D70748
Probable formamidopyrimidine-dna glycosylase - Mycobacterium tuberculosis (strain H37Rv
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: D70748
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70748
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-289 <COL>
A;Cross-references: GB:274697; GB:AL123456; NID:g3261602; PIDN:CAA98987.1; PID:g3261604
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: fpg
C;Superfamily: formamidopyrimidine-DNA glycosylase

Query Match 5.0%; Score 7; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DVMREAL 29
| | | | |
DB 219 DVMREAL 225

RESULT 11
AH0552
protein-export membrane protein SecF [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0552
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulie, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Paratyphi A
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08864.1; PID:g16501677; GSPDB:GN00176
C;Genetics:
A;Gene: STY0446
C;Superfamily: Escherichia coli preprotein translocase chain secF

Query Match 5.0%; Score 7; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DVMREAL 29
| | | | |
DB 69 DVMREAL 75

RESULT 12
G83517
probable glycosyl transferase PA1014 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83517
R;Scover, C.K.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: AB2950; MUID:20437337; PMID:10984043
A;Accession: G83517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <STO>
A;Cross-references: GB:AE004534; GB:AE004091; NID:g9946924; PIDN:AA04403.1; GSPDB:GN00176
A;Experimental source: strain PA01
C;Genetics:

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 STSTTTN 9
|||||

Db 45 STSTTTN 51

RESULT 15
B83303
phenylalanyl-tRNA synthetase, alpha-subunit PA2740 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83303
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10994043
A:Accession: B83303
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <STO>
A:Cross-references: GB:AE004702; GB:AE004091; NID:G9948813; PIDN:AA06128.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: pheS; PA2740
C:Superfamily: phenylalanine-tRNA ligase alpha chain

Query Match 5.0%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERLAMLR 42
|||||

Db 311 ERLAMLR 317

RESULT 16
T34158
hypothetical protein C42D4.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34158
R:Du, Z.; Le, T.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid C42D4.
A:Reference number: Z21483
A:Accession: T34158
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-339 <DUZ>
A:Cross-references: EMBL:U41991; PIDN:AAA83342.1; CESP:C42D4.6
C:Genetics:
A:Gene: CESP:C42D4.6
A:Introns: 135/1; 158/3

Query Match 5.0%; Score 7; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 RKIREMN 98
|||||

Db 79 RKIREMN 85

RESULT 17
S22356
phenylalanine-tRNA ligase (EC 6.1.1.20) alpha chain [validated] - Thermus aquaticus
N:Alternate names: phenylalanyl-tRNA synthetase alpha chain
C:Species: Thermus aquaticus
C>Date: 22-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 03-Jun-2002
C:Accession: S22356; S25717; S61093; T52502; S21468

R;Keller, B.; Kast, P.; Hennecke, H.
FEBS Lett. 301, 83-88, 1992
A:Title: Cloning and sequence analysis of the phenylalanyl-tRNA synthetase genes (pheST
A:Reference number: S22366; MUID:93083630; PMID:1451792
A:Accession: S22366
A:Molecule type: DNA
A:Residues: 1-350 <KEL>
A:Cross-references: EMBL:Z12118; NID:G48253; PIDN:CAA78104.1; PID:G48254
A:Note: the source is designated as Thermus thermophilus
R;Kreutzer, R.; Kruff, V.; Bobkova, E.V.; Lavrik, O.I.; Sprinzl, M.
Nucleic Acids Res. 20, 4173-4178, 1992
A:Title: Structure of the phenylalanyl-tRNA synthetase genes from Thermus thermophilus
A:Reference number: S25717; MUID:92375722; PMID:1508711
A:Accession: S25717
A:Molecule type: DNA
A:Residues: 1-350 <KRE>
A:Cross-references: EMBL:X65609; NID:G48250; PIDN:CAA46559.1; PID:G48251
A:Experimental source: strain HB8 (ATCC 27634)
A:Note: the source is designated as Thermus thermophilus
A:Accession: S61093
A:Molecule type: protein
A:Residues: 1-29 <KRW>
R;Lechler, A.; Kreutzer, R.
J. Mol. Biol. 278, 897-901, 1998
A:Title: The phenylalanyl-tRNA synthetase specifically binds DNA.
A:Reference number: Z26096
A:Accession: T52502
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-350 <LEC>
A:Cross-references: EMBL:Y15464; PIDN:CAA75644.1
A:Experimental source: strain HB8
C:Genetics:
A:Gene: pheS
C:Function:
A:Description: EC 6.1.1.20 [validated, MUID:98263257]; binds specifically certain DNA s
C:Superfamily: phenylalanine-tRNA ligase alpha chain
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 5.0%; Score 7; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERLAMLR 42
|||||

Db 320 ERLAMLR 326

RESULT 18
S45887
ribosomal protein L4.e.A, cytosolic - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR0315; protein YBR031w; ribosomal protein rp2; ribosomal p
C:Species: Saccharomyces cerevisiae
C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 13-Aug-1999
C:Accession: S45887; S46561; A28656; S45500
R;Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45875
A:Accession: S45887
A:Molecule type: DNA
A:Residues: 1-362 <GRI>
A:Cross-references: EMBL:Z35900; NID:G536243; PIDN:CAA84973.1; PID:G536244; MIPS:YBR031
A:Experimental source: strain S288C
R;Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
Yeast 10(Suppl.A), S75-S80, 1994
A:Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II fr
ly identified genes and a homologue of the SCO1 gene.
A:Reference number: S46551; MUID:94378725; PMID:8091864
A:Accession: S46561
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <SMI>
A:Cross-references: EMBL:X76078; NID:G498748; PIDN:CAA53687.1; PID:G498759

A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
R;Presutti, C.; Lucifoli, A.; Borzoni, I.
J. Biol. Chem. 263, 6188-6192, 1988
A;Title: Ribosomal protein L2 in Saccharomyces cerevisiae is homologous to ribosomal protein L2 in Escherichia coli
A;Reference number: A28656; MUID:88198160; PMID:2834365
A;Accession: A28656
A;Molecule type: DNA
A;Residues: 1-37, 'L', 39-143, 'T', 145-156, 'D', 158-223, 'S', 225-240, 'S', 242-362 <PRE>
A;Cross-references: GB:J03195; NID:gl216215; PIDN:AAA4974.1; PID:gl216215
A;Note: the authors translated the codon CAA for residue 59 as Glu and CAC for residue 3 as Gln
R;Takahara, H.; Tsunashima, S.; Miyagi, M.; Warner, J.R.
J. Biol. Chem. 267, 5442-5445, 1992
A;Title: NH2-terminal acetylation of ribosomal proteins of Saccharomyces cerevisiae.
A;Reference number: S45500; MUID:92184799; PMID:1544921
A;Accession: S45500
A;Molecule type: protein
A;Residues: 2-21 <TAK>
C;Genetics:
A;Gene: SGD:YBR031W
A;Cross-references: SGD:S0000235; MIPS:YBR031W
A;Map position: 2R
A;Superfamily: rat ribosomal protein L4
C;Keywords: acetylated amino end; blocked amino end; cytosol; protein biosynthesis; ribosomal protein L4
F;2/362/Product: ribosomal protein L4.e #status experimental <MAT>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 5.0%; Score 7; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 ASATAAT 64
|||||
DB 123 ASATAAT 129

RESULT 19
S50993
Ribosomal protein L4.e.B. cytosolic - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D3221; protein P2B362; protein Y8B119.17; protein Y8B122w; ribosomal protein L4.e.B.
C;Species: Saccharomyces cerevisiae
C;Date: 11-Feb-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C;Accession: S50993; S63419; S42260; S67825; S72110
R;Murphy, L.; Richards, C.; Gentles, S.; Harris, D.
submitted to the EMBL Data Library, January 1995
A;Reference number: S50976
A;Accession: S50993
A;Molecule type: DNA
A;Residues: 1-362 <MUR>
A;Cross-references: EMBL:Z48008; NID:9642799; PIDN:CAA88072.1; PID:g642817
R;Eide, L.G.; Sander, C.; Prydz, H.
submitted to the EMBL Data Library, February 1996
A;Description: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome 10
A;Reference number: S63416
A;Accession: S63419
A;Molecule type: DNA
A;Residues: 1-362 <EID>
A;Cross-references: EMBL:X95966; NID:gl216215; PIDN:CAA65204.1; PID:gl216219
R;Presutti, C.
submitted to the EMBL Data Library, February 1989
A;Reference number: S42260
A;Accession: S42260
A;Molecule type: DNA
A;Residues: 1-87, 'R', 89-200 <PRE>
A;Cross-references: EMBL:J22583; NID:gl216215; PIDN:AAA34975.1; PID:g553139
R;Prydz, H.; Eide, L.G.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67825
A;Accession: S67825
A;Molecule type: DNA
A;Residues: 1-362 <PRY>
A;Cross-references: EMBL:Z74308; NID:gl431431; PIDN:CAA98832.1; PID:gl431432; MIPS:YDR014
A;Experimental source: strain S288C

R;Eide, L.G.; Sander, C.; Prydz, H.
Yeast 12, 1085-1090, 1996
A;Title: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV
A;Reference number: S72107; MUID:97051598; PMID:8896275
A;Accession: S72110
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-362 <EID>
A;Cross-references: EMBL:X95966; NID:gl216215; PIDN:CAA65204.1; PID:gl216219
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Genetics:
A;Gene: SGD:RPL2B
A;Cross-references: MIPS:YDR012w; SGD:S0002419
A;Map position: 4R
C;Superfamily: rat ribosomal protein L4
C;Keywords: cytosol; protein biosynthesis; ribosome

Query Match 5.0%; Score 7; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 ASATAAT 64
|||||
DB 123 ASATAAT 129

RESULT 20
BVBYK2
MAK32 protein - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YCR019w
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1991 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
C;Accession: S19429; S07695
R;Feldmann, H.; Mannhaupt, G.; Vetter, I.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19429
A;Accession: S19429
A;Molecule type: DNA
A;Residues: 1-363 <FEU>
A;Cross-references: EMBL:X59720; NID:gl907116; PIDN:CAA42310.1; PID:gl907162; GSPDB:GN
R;Tob-e, A.; Sanashi, Y.
Yeast 11, 159-171, 1985
A;Title: The PET18 locus of Saccharomyces cerevisiae: a complex locus containing multiple
A;Reference number: S07692; MUID:89131254; PMID:3916862
A;Accession: S07695
A;Molecule type: DNA
A;Residues: 1-14, 'I', 15-81, 83-282, 'S', 284-363 <TOH>
C;Genetics:
A;Gene: SGD:MAK32; MIPS:YCR019w
A;Cross-references: SGD:S0000612; MIPS:YCR019w
A;Map position: 3R
C;Superfamily: MAK32 protein

Query Match 5.0%; Score 7; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LLRVKSS 35
|||||
DB 158 LLRVKSS 164

RESULT 21
AD1188
membrane proteins homolog lmo0908 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1188
R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloechl
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, I.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;